

GenCore version 4.5
 Copyright (c) 1993 - 2000 compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:10 ; Search time 34.79 Seconds
 (without alignments) updates/sec 592.474 Million cell/sec

Title: US-09-492-029-3
 Perfect score: 1809
 Sequence: MGEMQLKOEAEQIKKQIAD.....TADGMNAVATGSWDSFLKIWN 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database :
 1: A_Geneseq_0601.*
 2: /SIDS8/gcadata/geneseq/geneseq/AA1980.DAT:/*
 3: /SIDS8/gcadata/geneseq/geneseq/AA1982.DAT:/*
 4: /SIDS8/gcadata/geneseq/geneseq/AA1983.DAT:/*
 5: /SIDS8/gcadata/geneseq/geneseq/AA1986.DAT:/*
 6: /SIDS8/gcadata/geneseq/geneseq/AA1987.DAT:/*
 7: /SIDS8/gcadata/geneseq/geneseq/AA1988.DAT:/*
 8: /SIDS8/gcadata/geneseq/geneseq/AA1989.DAT:/*
 9: /SIDS8/gcadata/geneseq/geneseq/AA1990.DAT:/*
 10: /SIDS8/gcadata/geneseq/geneseq/AA1991.DAT:/*
 11: /SIDS8/gcadata/geneseq/geneseq/AA1992.DAT:/*
 12: /SIDS8/gcadata/geneseq/geneseq/AA1993.DAT:/*
 13: /SIDS8/gcadata/geneseq/geneseq/AA1994.DAT:/*
 14: /SIDS8/gcadata/geneseq/geneseq/AA1995.DAT:/*
 15: /SIDS8/gcadata/geneseq/geneseq/AA1996.DAT:/*
 16: /SIDS8/gcadata/geneseq/geneseq/AA1997.DAT:/*
 17: /SIDS8/gcadata/geneseq/geneseq/AA1998.DAT:/*
 18: /SIDS8/gcadata/geneseq/geneseq/AA1999.DAT:/*
 19: /SIDS8/gcadata/geneseq/geneseq/AA2000.DAT:/*
 20: /SIDS8/gcadata/geneseq/geneseq/AA2001.DAT:/*
 21: /SIDS8/gcadata/geneseq/geneseq/AA2002.DAT:/*
 22: /SIDS8/gcadata/geneseq/geneseq/AA2003.DAT:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID Description

No. Score Rat Taste Cell spe

1 1809 100.0 340 21 AAB15168 Mutant rat Taste C

2 1806 99.8 340 21 AAB15170 Mutant rat Taste C

3 1806 99.8 340 21 AAB15171 Mutant rat Taste C

4 1805 99.8 340 21 AAB15172 Human G protein b

5 1762 97.4 340 21 AAB15169 Human Taste Cell

6 1762 97.4 340 21 AAB15173 Human Rgb3 G-prot

7 1760 97.3 340 21 AAB15174 Mutant human Taste

8 1759 97.2 340 21 AAB15175 Mutant human Taste

9 1759 97.2 340 21 AAB15176 WD-40 domain-contg

10 1759 97.2 340 21 AAB15177 WD-40 domain-contg

11 1753 87.0 340 21 AAY67863 WD-40 domain-contg

12 1573 84.2 340 16 AAR85863 Human Hgb2 G-prot

13 1523 84.2 340 21 AY67864 Human G-protein be

14 1520.5 84.1 299 19 AAW9364 Human G-protein be

15 1518.5 83.9 297 21 AAY67866 Mouse Mgb2 G-prot

16 1493 82.5 340 21 AAY67866 WD-40 domain-contg

17 1467 81.1 340 16 AAR85861 WD-40 domain-contg

18 1452 80.3 340 16 AAR85860 Human cell cycle r

19 1419 78.4 326 20 AAY31732 Human Mgb5 G-Prot

20 946.5 52.3 395 20 Human pancreatic c

21 945.5 52.3 353 21 AAY67867 Gene 45 human secr

22 901.5 49.8 371 21 AAB54247 Human secreted pro

23 863.5 47.7 295 22 AAB75330 Arabidopsis thalia

24 860.5 47.6 295 22 AAB75315 Gene 45 human secr

25 817.7 45.2 229 22 AAB75332 Arabidopsis thalia

26 655.5 36.1 267 21 AAG16503 Arabidopsis thalia

RESULT

1 ID AAB15168 standard; Protein: 340 AA.

XX AC AAB15168;

XX DT 12-DEC-2000 (first entry)

XX DE Rat Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;

XX KW Rat; Taste Cell specific G-protein beta 3 subunit; food industry;

XX OS Rattus sp.

XX PN WO20045179-A2.

XX PD 03-AUG-2000.

XX PF 26-JAN-2000; 2000WO-US02218.

XX PR 27-JAN-1999; 99US-0117404.

XX PR (REC) UNIV CALIFORNIA.

XX PI Zuker CS, Adler JE, Lindemeyer J;

XX DR WPI; 2000-499361/44.

XX N-PDB; AAB47490.

Human Hobb1 G-prot
 WD-40 domain-contg
 Human Hgb2 G-prot
 Human G-protein be
 Human G-protein be
 Mouse Mgb2 G-prot
 WD-40 domain-contg
 Arabidopsis thalia
 Gene 45 human secr
 Arabidopsis thalia
 Arabidopsis thalia
 Arabidopsis thalia
 Human secreted pro
 WD-40 domain-contg
 Arabidopsis thalia
 Ste4p/Gbeta intera
 Yeast G protein be
 Yeast G protein be
 Yeast Ste4 protein
 Human secreted pro
 Breast and ovarian
 Human cancer assoc
 Arabidopsis thalia
 Arabidopsis thalia
 Arabidopsis thalia
 Human GIP-binding
 Arabidopsis thalia
 Arabidopsis thalia
 Arabidopsis thalia

XX
 RS . Claim 1; Page 62; 68pp; English.
 CC The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is
 CC expressed specifically in taste cells, hence this sequence is referred to
 CC as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is
 CC involved in the taste transduction pathway. TC-Gbeta3 may be used for
 CC pharmaceutical and food industries to customise taste.
 XX SQ Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.2e-170; Mismatches 0; Indels 0; Gaps 0;
 Matches 340; Conservative 0; MisMatches 0; Del 0; Insert 0; PT
 QY 1 NGEMQQLQKQEAQTKQDARKACADITLAELVSLGLEVGRVOMRTRTLRGLAKIYA 60
 Db 1 mgemeqkqeaedkkqkqadarkacaditlaelvslglevgrvomrtrtlrglakiya 60
 CC
 QY 61 MHWATDSKLVLVSAASODGKLIVWPTYTINKHAIPLRSSWMTCAYAASGGNVAACGLDNM 120
 Db 61 mhwatsklvlvasqgkliwvdtytinkhailplrsswmmtcayapsgnvaacgldnm 120
 CC
 QY 121 CSYISLKSREGNVKVSRELSAHGFLSCRFEDDNNTVSSGDTCAWLWDETOQKTVF 180
 Db 121 csyislkssregnkvksrelsahgflscrfednnntvssgdtcawlwdeitoqktvf 180
 CC
 QY 181 VGHGDCMSLAVSPQPKURISGCDASAKLWVREGTCRGTGHESDNDNAICEFNGEA 240
 Db 181 vghtgdcmslavspqpkurisgcdasaklwvregtcrgtghesdndnaicefngea 240
 CC
 QY 241 ICGSDDASCRFLDRADQELTAYSHESITCGTSAFSLSGRILFAGYDDENCNWDSL 300
 Db 241 ictgsddascrifldradqeltayshesitcgtsafsllfagydencnwdsi 300
 CC
 QY 301 KERVGVGLSGHDNRVSGLVTAADGMWAVGSMWDFSLKIWN 340
 Db 301 kcervgvlsghdnrvsclytgtaadgmavatgswdfslkiwn 340
 XX SQ Sequence 340 AA;

Query Match 99.8%; Score 1806; DB 21; Length 340;
 Best Local Similarity 99.8%; Pred. No. 1e-169; Mismatches 0; Indels 0; Gaps 0;
 Matches 339; Conservative 1; MisMatches 0; Del 0; Insert 0; PT
 QY 1 MGEMQQLQKQEAQTKQDARKACADITLAELVSLGLEVGRVOMRTRTLRGLAKIYA 60
 Db 1 mgemeqrqeaekkkqkqadarkacaditlaelvslglevgrvomrtrtlrglakiya 60
 CC
 QY 61 MHWATDSKLVLVSAASODGKLIVWPTYTINKHAIPLRSSWMTCAYAASGGNVAACGLDNM 120
 Db 61 mhwatsklvlvasqgkliwvdtytinkhailplrsswmmtcayapsgnvaacgldnm 120
 CC
 QY 121 CSYISLKSREGNVKVSRELSAHGFLSCRFEDDNNTVSSGDTCAWLWDETOQKTVF 180
 Db 121 csyislkssregnkvksrelsahgflscrfednnntvssgdtcawlwdeitoqktvf 180
 CC
 QY 181 VGHGDCMSLAVSPQPKURISGCDASAKLWVREGTCRGTGHESDNDNAICEFNGEA 240
 Db 181 vghtgdcmslavspqpkurisgcdasaklwvregtcrgtghesdndnaicefngea 240
 CC
 QY 241 ICGSDDASCRFLDRADQELTAYSHESITCGTSAFSLSGRILFAGYDDENCNWDSL 300
 Db 241 ictgsddascrifldradqeltayshesitcgtsafsllfagydencnwdsi 300
 CC
 QY 301 KERVGVGLSGHDNRVSGLVTAADGMWAVGSMWDFSLKIWN 340
 Db 301 kcervgvlsghdnrvsclytgtaadgmavatgswdfslkiwn 340
 XX SQ Sequence 340 AA;

RESULT 2
 ID AAB15170
 AC AAB15170;
 XX
 DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
 XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 XX mutein; mutant.
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /note= "Wild-type Lys substituted by Arg"
 XX
 PN WO20045179-A2.
 XX
 PD 03-AUG-2000.
 XX PF 26-JAN-2000; 2000WO-US02218.
 XX PR 27-JAN-1999; 99US-011704.
 XX PA (RECC) UNIV CALIFORNIA.
 XX

RESULT 3
 ID AAB15171
 AC AAB15171;
 XX
 DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #2.
 XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 XX mutein; mutant.
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 12 /note= "Wild-type Glu substituted by Asp"
 XX

PI zuker CS, Adler JE, Lindemeier J;
 XX DR WPI; 2000-499361/44.
 CC Identifying a compound that modulates sensory signaling in sensory
 CC cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX SQ Disclosure: Page 7; 68pp; English.
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 be used for identifying taste modulating compounds which can be used in
 pharmaceutical and food industries to customise taste.
 Note: The present sequence is not shown in the specification but is
 derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 AAB15168) and information given on page 8 of the disclosure.

PI zuker CS, Adler JE, Lindemeier J;
 XX DR WPI; 2000-499361/44.
 CC Identifying a compound that modulates sensory signaling in sensory
 CC cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX SQ Disclosure: Page 7; 68pp; English.
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 be used for identifying taste modulating compounds which can be used in
 pharmaceutical and food industries to customise taste.
 Note: The present sequence is not shown in the specification but is
 derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 AAB15168) and information given on page 8 of the disclosure.

Fri Sep 28 10:45:04 2001

RESULT 5
 ID AAW36598
 XX AAW36598 standard; Protein: 340 AA.
 AC AAW36598;
 XX
 DT 19-MAY-1998 (first entry)
 DE Human G protein beta-3 subunit.
 KW Protein beta-3 subunit; variant; mutation; hypertension; diagnosis;
 KW cardiovascular disease; metabolic disorder; immunological disorder.
 OS Homo sapiens.
 PN DE19610362-A1.
 XX
 PD 20-NOV-1997.
 XX
 PF 14-MAY-1996; 96DE-1019362.
 PR 14-MAY-1996; 96DE-1019362.
 PA (BADI) BASF AG.
 XX
 PI Siffert W;
 XX
 DR WPI; 1998-000675/01.
 DR N-PSDB; AAT96746; AAV09741.
 PT Assessing risk of disease, especially hypertension - by detecting mutation in human G-protein beta-3 sub:unit gene
 PS Claim 3: Page 6; 8pp; German.
 XX
 CC This sequence represents the human G-protein beta 3 subunit. A variant of the gene encoding this protein has applications in the diagnosis of diseases or assessing the risk of a disease associated with G-protein misregulation. G-protein misregulation is associated with hypertension, cardiovascular diseases e.g. coronary heart disease, atherosclerosis, diabetic complications, disorders of lipid metabolism and central chemoreception dysfunction (e.g. sudden infant death syndrome), and immunological disorders such as diabetes, cirrhosis and transplant rejection.
 CC
 CC Sequence 340 AA;

Query Match 97.4%; Score 1762; DB 19; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2.3e-165; Mismatches 8; Indels 0; Gaps 0;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGEMEQIKQEAEQQLKQIADARKACADITLAELVSGLEVVGRYQMRRTLGHAKIYA 60
 Db 1 mgemeqikqeqgeaqkqkqiadarkakadvtaelvsglevgrvgrmrtrtirghakiya 60
 QY 61 MHWATDSKLVLVSASQDGKLIWDTTNTKYHAIPRLSSWMTCAYAAPSGLNFWACGGIDNM 120
 Db 61 mhawatdsklvlvsasqdgkliwvdtyttkvhaplrswwmtcavapsgnfvacggidnm 120
 QY 121 CSYTSIKSREGNVKYSRELSAHTGYLSCRFEDDDNNIVTSSDITCRLWDIETGQKRTVF 180
 Db 121 csiytsikskregnvksrelsahtgylscrfedddnnivtssdttcalwdietgqkrtvf 180
 QY 181 VGHTEGDCMSLAVSPDYKUFIGSADASKLWVRESCICPQFTGHSNDINACFPNGEA 240
 Db 181 vghtedcmslavspdnifisgacdasaklwvregtcrcqftgnsedinaicfpngea 240
 QY 241 ICTSSDDASCRFLPDRALQELTAYSHISIGITSAFSISGRLLFAGYDFDENVNWL 300
 Db 181 vghedcmslavspdnifisgacdasaklwvregtcrcqftgnsedinaicfpngea 240

RESULT 6
 ID AAB15169
 XX AAB15169 standard; Protein: 340 AA.
 AC AAB15169;
 XX
 DT 12-DEC-2000 (first entry)
 DE Human Taste Cell specific G-protein beta 3 subunit.
 XX
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry.
 OS Homo sapiens.
 PN WO200045170-A2.
 XX
 PD 03-AUG-2000.
 XX
 PP 26-JAN-2000; 2000WO-US02218.
 PR 27-JAN-1999; 99US-0117404.
 PA (REGC) UNIV CALIFORNIA.
 PT zuker CS, Adler JE, Lindemeier J;
 XX
 DR WPI; 2000-499361-44.
 DR N-PSDB; AAA4591.
 XX
 PT Identifying a compound that modulates sensory signaling in sensory cells for use in pharmaceutical and food industries comprises PT contacting the compound with a sensory cell specific G-protein beta polypeptide -
 XX
 PS Claim 1: Page 63; 6pp; English.
 CC The present sequence is human G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit ($\text{TC-G}\beta_3$). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.
 XX
 SQ Sequence 340 AA;

Query Match 97.4%; Score 1762; DB 21; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2.3e-165; Mismatches 8; Indels 0; Gaps 0;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGEMEQIKQEAEQQLKQIADARKACADITLAELVSGLEVVGRYQMRRTLGHAKIYA 60
 Db 1 mgemeqikqeqgeaqkqkqiadarkakadvtaelvsglevgrvgrmrtrtirghakiya 60
 QY 61 MHWATDSKLVLVSASQDGKLIWDTTNTKYHAIPRLSSWMTCAYAAPSGLNFWACGGIDNM 120
 Db 61 mhawatdsklvlvsasqdgkliwvdtyttkvhaplrswwmtcavapsgnfvacggidnm 120
 QY 121 CSYTSIKSREGNVKYSRELSAHTGYLSCRFEDDDNNIVTSSDITCRLWDIETGQKRTVF 180
 Db 121 csiytsikskregnvksrelsahtgylscrfedddnnivtssdttcalwdietgqkrtvf 180
 QY 181 VGHTEGDCMSLAVSPDYKUFIGSADASKLWVRESCICPQFTGHSNDINACFPNGEA 240
 Db 181 vghtedcmslavspdnifisgacdasaklwvregtcrcqftgnsedinaicfpngea 240
 QY 241 ICTSSDDASCRFLPDRALQELTAYSHISIGITSAFSISGRLLFAGYDFDENVNWL 300
 Db 181 vghedcmslavspdnifisgacdasaklwvregtcrcqftgnsedinaicfpngea 240

Fri Sep 28 10:45:04 2001

QY	241	ICTGSSDASCRLEDLRAQELTAYSHESITICGITSVAFSLSGRLIFAGYDDFNQNWDSL	300	OY	121	CSRYSLKSREGNVKRSRELSAHTGILSCRCFLDDNNIVTSGDPTCALWDIETGQKTVF	180
Db	241	ictgssdascrlfdradqelicsfhesicqgtstafslsgrlifagydffcnwdsml	300	Db	121	cslynlksregnkvrsrelnsytysccrfldnnivssgdttcaldwetggqkfvf	180
OY	301	KCERYGVLSGDHNRVSCLGVTADGMATGSDSFKWN	340	OY	181	VGHGDCMSLAVSPDKYRISGAQDASKLWDVRECGRCFTGIESDNIAICFPNGEA	240
Db	301	kservgilsghdnrvsclgvtadgmavatgswdsflkiwn	340	Db	181	vghtgocmislavspdnflisggdasaklwdrregtcqrqtftgnesdniaicfpngea	240
RESULT	7			OY	241	ICTGSDASCRLEDLRAQELTAYSHESITICGITSVAFSLSGRLIFAGYDDFNQNWDSL	300
AN167865		standard; protein; 340 AA.		QY	301	KCERYGVLSGDHNRVSCLGVTADGMATGSDSFKWN	340
ID	AAY67865			Db	301	kservgilsghdnrvsclgvtadgmavatgswdsflkiwn	340
XX				Db	301	kservgilsghdnrvsclgvtadgmavatgswdsflkiwn	340
AC	AAY67865;			Db	301	kservgilsghdnrvsclgvtadgmavatgswdsflkiwn	340
XX				Db	301	kservgilsghdnrvsclgvtadgmavatgswdsflkiwn	340
DT	25-APR-2000	(first entry)		RESULT	8		
DE	Human Hgb3	G-protein beta3 subunit amino acid sequence.		ID	AAB15173		
XX				ID	AAB15173	standard; Protein; 340 AA.	
KW	Ste20p/PAK; G-protein-coupled receptor signal transduction; p21-activated protein kinase; G-protein coupled receptor signal transduction; Homo sapiens.			XX	AAB15173;		
XX				XX		12-DEC-2000 (first entry)	
OS	Homo sapiens.			DE		mutant human Taste Cell specific G-protein beta 3 subunit variant #1.	
XX				XX		Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3; taste transduction pathway; pharmaceutical; mutation; mutain; mutant.	
PN	CA2219958-A1.			KW			
XX				XX			
PD	07-JUL-1999.			XX			
XX				XX			
PF	07-JAN-1998;	98CA-2219958.		XX			
XX				XX			
PR	07-JAN-1998;	98CA-2219958.		XX			
XX				XX			
XX	(LEBE/)	LEBERER E.		XX			
PA	(LEBU/)	LEEUW T.		XX			
PA	(THOM/)	THOMAS D Y.		XX			
PA	(WHITE/)	WHITEWAY M.		XX			
XX				XX			
PI	Leberer E,	Leeuw T,	Thomas DY,	XX			
XX				XX			
DR	WPI: 2000-137553/13.			XX			
XX				XX			
PT	Interacting polypeptides involved in G-protein-coupled receptor signal transduction -			XX			
PT				XX			
XX				XX			
PS	Claim 3; Fig 6; 91pp; English.			XX			
XX				XX			
CC	This sequence represents the beta3 subunit of a human G-protein. The invention relates to the G-protein beta subunit interaction domain of the invention family of protein kinases. The Ste20p/PAK family of protein kinases are p21-activated protein kinases (PAK), and they are involved in many varied cellular processes ranging from morphogenesis and stress response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and Ste20p/PAK are useful for designing in vitro and in vivo experimental models which enable the screening of large collections of synthetic, semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta and Ste20p/PAK dependent diseases.		XX				
CC				XX			
SQ	Sequence 340 AA:			XX			
Query Match	97.4%	Score 1762; DB 21; Length 340;		XX			
Best Local Similarity	96.5%	Prod. No. 2.3e-165; Indels 0; Gaps 0;		XX			
Matches	328;	Conservative 8; Mismatches 4;		XX			
OY	1	MGEGBOLKOBAAEQLKQADARACACDITLEALWSLEEVGRQARTTRTLGHAKIYA	60	CC		The present sequence is a mutant human G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as taste Cell specific G-protein beta 3 subunit (TC-beta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.	
Db	1	ngemeqlrgaeaqikkqiqadaracacdtaelalwsleevgrqarttrtlghakiya	60	CC	Note: The present sequence is not shown in the specification but is derived from the human wild-type TC-Gbeta3 sequence given on page 63 (see AAB15169) and information given on page 8 of the disclosure.		
OY	61	MHWATSKLIVSASDQGKILWWDYPTTNKVHATPLRSSWWMCAYAPSGNWFACGLDM	120	CC			
Db	61	mhwatdklivilsasdqgkiliwdsytrkvhapirsswmccayapsgnwfacgldm	120	XX			

CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC TC-Gbeta3 may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.

SQ Sequence 340 AA;

XX

CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC TC-Gbeta3 may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.

SQ Sequence 340 AA;

XX

AC AAB15174;
 AC
 XX
 DT 12-DEC-2000 (first entry)
 XX
 DE Mutant human taste Cell specific G-protein beta 3 subunit variant ;
 XX Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 XX muttein; mutant.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH location/Qualifiers
 FT Key-difference 161
 FT /note= "Wild-type Ser substituted by Thr"
 XX WO20045179-A2.
 PN
 XX PD 03 - AUG - 2000.
 XX PF 26 - JAN - 2000; 2000WO-US02218.
 XX PR 27 - JAN - 1999; 99US-0117404.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI zuker CS, Adler JE, Lindemeyer J;
 XX DR WPI; 2000-49361/44.
 PT identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 PT Disclosure; Page - ; 68pp; English.
 CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC G-protein beta 3 is expressed specifically in taste cells, hence this
 CC

QY	241	ICTGSDPDAASRLFLDRADELTAVSHEEICIGTSVAFSLSGRLIFAGYDDFNWCNWDSL	240
Db	241	ictgdedasrcifldraagelcifshaeicitsrassgrlfagydafnchowdsm	300
QY	301	KCERVGVLSGHNDNRVSCIGVTADGMATVGSMDSFKIKW	340
Db	301	kservgvlsghndrvscigvtadgmavatgswstfkikw	340
RESULT	10		
AAB15175			
ID	AAB15175	standard; Protein: 340 AA.	
XX			
AC	AAB15175;		
XX			
DT	12-DEC-2000	(first entry)	
XX			
DE	Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.		
XX			
KW	Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;		
KW	taste transduction pathway; pharmaceutical; food industry; mutation;		
KW	muttein; mutant,		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	301	
FT		/note= "Wild-type Lys substituted by Arg"	
XX			
PN	WO200045179-A2.		
XX			
PD	03-AUG-2000.		
XX			
PF	26-JAN-2000; 2000WO-US02218.		
XX			
PR	27-JAN-1999; 99US-0117404.		
PA	(REGC) UNIV CALIFORNIA.		
XX			
PI	Zuker CS, Adler JE, Lindemeyer J;		
XX			

DR	WPI: 2000-499361/44.	PR	01-FEB-1994; 94US-0190802.
XX	Identifying a compound that modulates sensory signaling in sensory	PT	(STRD) UNTV LELAND STANFORD JUNIOR.
PT	cells for use in pharmaceutical and food industries comprises	PA	Mochly-Rosen D, Ron D;
PT	contacting the compound with a sensory cell specific G-protein beta	XX	
PT	peptide -	XX	
XX		DR	WPI: 1995-283772/37.
PS	Disclosure: Page :-; 68PP; English.	XX	
CC	The present sequence is a mutant human G-protein beta 3 subunit.	PT	New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
CC	G-protein beta 3 is expressed specifically in taste cells, hence this	PT	activity of a protein, eg. protein kinase C, which interacts with a
CC	sequence is referred to as Taste Cell specific G-protein beta 3 subunit	PT	protein contg. a WD-40 region.
CC	(TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.	XX	Example 5; Page 102-103; 351PP; English.
CC	TC-Gbeta3 may be used for identifying taste modulating compounds which	XX	
CC	can be used in pharmaceutical and food industries to customise taste.	CC	Proteins AAR85851-92 are protein which contain at least one WD-40 (also
CC	Note: The present sequence is not shown in the specification but is	CC	called beta-transducing homologous) amino acid repeat motifs. The WD-40
CC	derived from the human wild type TC-Gbeta3 sequence given on page 63	CC	regions are involved in protein-protein interactions between proteins
CC	(see AAB15169) and information given on page 8 of the disclosure.	CC	involved in intracellular signalling. An example of such an interaction
XX	Sequence 340 AA;	CC	is between protein kinase C and receptors of activated protein kinase
SQ	Query Match 97.2%; Score 1759; DB 21; Length 340;	CC	(RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
	Best Local Similarity 96.2%; Pred. No. 4; 4e-165;	CC	on homology with beta-transducin, whereas proteins AAR85882-92 were
	Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;	CC	isolated based on homology with the WD-40 consensus sequence (AAR85993).
Db	1 mgeneqrleaqeqkqiadarkacadvatlaelvsglevygrvgmrtrrtirghlakiya 60	CC	The proteins were used to construct the peptides AAR8428-885063 and
QY	61 MHWATDSKLUVSASQDGKLIWDTTYTNKWHAPLRLSSWMTCAVAFSGNFVAGGLDM 120	CC	AAR8576-RB5842. The peptides can be used to identify target proteins
Db	61 mbwatsdkluvsasqdgkliwdsyttkvhaplrlsswmtcavafsgnfvacggldm 120	CC	contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
QY	121 CSIVSLSKSRREGNVKVSRELSAHTGTYLSCRCRFLDDNNIVTSSGGNTCALWDIETGQKTVF 180	CC	proteins involved in protein-protein interaction and to screen for drugs
Db	121 csivnltksregnkvksrelsahgtgylscrcflddnnitssggattcalwdietgqktvf 180	CC	that will affect protein-protein interaction involving WD-40 domains.
QY	181 VGHGDCMSLAVSVDYKLUISGACDASKLWDREGTORQTFGHESESINATCFFPNEA 240	XX	Sequence 340 AA;
Db	181 vghgdcmsslavspdnlfisgacdasaklwdvrgtcrqftfghesdinalccffpngea 240		
QY	241 ICGSSDDASCRFLRADQELTAYSHESICGITSVATSLSGRLLAGFYDDEFCNCNWDSL 300		
Db	241 ictgsddascrflradqelcifshesicgitsvatlslgllfagydffcnvwds 300		
QY	301 KCERVGVLSGDHNRVSCUGTAGMAMAVATGGSWDSFLKIWN 340		
Db	301 rservgilsghdnrvscigvtadgnmavatgswdsflkiwn 340		
RESULT 11	AAR85859		
ID	AAR85859 standard; Peptide; 340 AA.		
XX			
AC	AAR85859;		
XX			
DT	13-SEP-1996 (first entry)		
XX			
DE	WD-40 domain-contg. bovine G-beta-1 protein.		
XX			
KW	WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signaling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.		
XX			
OS	Bos taurus.		
XX			
PN	WO9521252-A2.		
XX			
PD	10-AUG-1995.		
XX			
XX	31-JAN-1995; 95WO-US01210.		
XX			
RESULT 12			
AAV67863			
ID	AAV67863 standard; protein; 340 AA.		
XX			
AC	AAV67863;		
XX			
DT	25-APR-2000 (first entry)		
XX			
DE	Human Hgbbl G-protein beta subunit amino acid sequence.		
XX			
KW	St20p/PAK; G-protein-coupled receptor signal transduction; human; Hgbbl; Stc4p/Gbeta		
KW	Stc4p/Gbeta interaction domain; P21-activated protein kinase; G-protein coupled receptor signal transduction;		

Fri Sep 28 10:45:04 2001

|||||||||||||||||:|||||||||||||||||:|||||||||||||||||:|||||||||||||||||:
Db 61 mhratdkllvysasdgkllwdsyrttnkyhaiprlsswmtcayapsgnfvacgg1.dmm 120
Qy 121 CSYSLKSREGAVKVSRBELSAHTGILSCCRFLDDNNITVSSGOTCAWDTENGQKTVF 180
|||:|||||||||:|||||||||:|||||||||:|||||||||:
Db 121 csiymlksregnkvksrelehtgysccrflldnnivessgatc----- 166
Qy 181 VGHNGDCMSLAVSPDYKLFIISGACDASAKWDVRGTCROTFIGHESDINATCFPPNGEA 240
|||:|||||||||:|||||||||:
Db 167 ----- 199
|||:|||||||||:
Qy 241 ICIGSDDASCRFLRADQELTAYHSBICIGITSVAFSISGRLLFAGYDDFNWNDSL 300
|||:|||||||||:
Db 200 ictsdasocrflradqelicsnesicqitvafslsgrillfagyddfnwnwasm 259
Qy 301 KCERVGVLSGHDNRYSCIGYTAGMAYATGSMDFETKWN 340
|||:|||||||||:
Db 260 kservgilsghdnrvscigvtadgmavatgswdssfikwn 299

Search completed: September 28, 2001, 10:29:21
Job time: 71 sec

us-09-492-029-3.rai

Fri Sep 28 10:45:05 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:09 ; Search time 20.71 seconds
(without alignments) updates/sec 338.036 Million cell updates/sec

Title: US-09-492-029-3

Perfect score: 1

Sequence: MGEMEQLKQEAQQLKKQIAD.....TADGMATGWSWDSLKTMN 340

Scoring table: BLOSUM62

Gapopt 10.0 , Gapext 0.5

Searched: 197339 seqs., 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Issued_Patents_AAI,*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.Frep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

RESULT 1 -2

US-09-180-783-2 Application US/09180783

; Sequence 2, 6242181

; Patent No.

; General Information:

; APPLICANT: Siffert, Winfried

; TITLE OF INVENTION: G PROTEIN b3 SUBUNIT FOR THE DIAGNOSIS OF DISEASES

; FILE REFERENCE: 1135-2

; CURRENT APPLICATION NUMBER: US/09/180, 783

; PRIORITY FILING DATE: 1999-03-17

; PRIORITY APPLICATION NUMBER: PCT/EP97/02250

; PRIOR FILING DATE:

; PRIORITY FILING DATE: 1997-05-02

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 2

; LENGTH: 340

; TYPE: PRTR

; ORGANISM: Homo sapiens

; US-09-180-783-2

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

Db 301 KSERVGLSLGHDRNVSCLGVTADGMATGSWDSFLKTNW 340

RESULT 2

US-08-190-802A-38

; Sequence 38, Application US/08190802A

; Patent No. 5519003

GENERAL INFORMATION:

; APPLICANT: Mochny-Rosen, Daria

; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: P.O. Box 60850

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94305-0850

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Pattern Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 8600-0139

; FILING DATE: 01-FEB-1994

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 340 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21

; US-08-190-802A-38

Query Match
Best Local Similarity 87.0%; Score 1573; DB 1; Length 340;
Matches 263; Conservative 83.2%; Pred. No. 1.e-153; Indels 0; Gaps 0;

QY 1 MGEMEOLKQEAQDQKQIADARKACADITLAEVLSPLEVIGVRVOMTRTGLHLAKIYA 60

Db 1 MSELQDOLRQEAEQKLNOIRDARKACADATLSQTINNIDPVGRITMRTRTGLHLAKIYA 60

QY 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLRSWMTGAYAPSGNFVACSGCLDNM 120

Db 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLRSWMTGAYAPSGNFVACSGCLDNM 120

QY 121 CSYSLSKREGNVKVSRELSAHTGTLSCRCRFDDNNINTSSGDTTALWDIETSGQKTVF 120

Db 121 CSYSLSKREGNVKVSRELSAHTGTLSCRCRFDDNNINTSSGDTTALWDIETSGQKTVF 120

QY 181 VGHGDCMSLAVSPDKLFTSGACDAKLDWRESTCRQFTGHESDINAICFPNGEA 180

Db 181 VGHGDCMSLAVSPDKLFTSGACDAKLDWRESTCRQFTGHESDINAICFPNGEA 180

QY 241 IGTGSDASURFLDRAOELTAYASHSIIIGTSFAFSISGRLLFGAGYDDCNWDSL 300

Db 241 IGTGSDASURFLDRAOELTAYASHSIIIGTSFAFSISGRLLFGAGYDDCNWDSL 300

QY 301 KCERVGLSLGHDRNVSCLGVTADGMATGSWDSFLKTNW 340

Db 301 KADRAYLAGHIDNRVSCLGVTADGMATGSWDSFLKTNW 340

RESULT 3

US-08-190-802A-42

; Sequence 42, Application US/08190802A

; Patent No. 5519003

GENERAL INFORMATION:

; APPLICANT: Mochny-Rosen, Daria

; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: P.O. Box 60850

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94305-0850

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Pattern Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,802A

; FILING DATE: 01-FEB-1994

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 340 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: G-Beta 2 (Human), Fig. 25
; US-08-190-802A-42Query Match
Best Local Similarity 84.2%; Score 1523; DB 1; Length 340;

Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMEOLKQEAQDQKQIADARKACADITLAEVLSPLEVIGVRVOMTRTGLHLAKIYA 60

Db 1 MSELQDOLRQEAEQKLNOIRDARKACADATLSQTINNIDPVGRITMRTRTGLHLAKIYA 60

QY 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLRSWMTGAYAPSGNFVACSGCLDNM 120

Db 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLRSWMTGAYAPSGNFVACSGCLDNM 120

QY 121 CSYSLSKREGNVKVSRELSAHTGTLSCRCRFDDNNINTSSGDTTALWDIETSGQKTVF 120

Db 121 CSYSLSKREGNVKVSRELSAHTGTLSCRCRFDDNNINTSSGDTTALWDIETSGQKTVF 120

QY 181 VGHGDCMSLAVSPDKLFTSGACDAKLDWRESTCRQFTGHESDINAICFPNGEA 180

Db 181 VGHGDCMSLAVSPDKLFTSGACDAKLDWRESTCRQFTGHESDINAICFPNGEA 180

QY 241 IGTGSDASURFLDRAOELTAYASHSIIIGTSFAFSISGRLLFGAGYDDCNWDSL 300

Db 241 IGTGSDASURFLDRAOELTAYASHSIIIGTSFAFSISGRLLFGAGYDDCNWDSL 300

RESULT 4
US-09-147-826B-2
; Sequence 2, application US/09147826B
; Patent No. 6,251,853
; GENERAL INFORMATION:
; APPLICANT: Siffert, Winfried
; TITLE OF INVENTION: PIX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE
; FILE REFERENCE: 1115-0003
; CURRENT APPLICATION NUMBER: US/09/147,826B
; CURRENT FILING DATE: 1999-03-15
; PRIORITY APPLICATION NUMBER: PCT/EP97/04709
; PRIORITY FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: DE 196 37 518.5
; PRIORITY FILING DATE: 1996-09-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-147-826B-2

Query Match 84.1%; Score 1520.5; DB 4; Length 299;
Best Local Similarity 85.0%; Pred. No. 3.2e-148;
Matches 289; Conservative 7; Mismatches 3; Indels 41; Gaps 1;

Qy 1 MGEMEQLKQEAQKKQIADARKACADITLAEVLGSLEVGRLVGRYOMRTRTLRGHLAKIYA 60
Db 1 MGEMEQLKQEAQKKQIADARKACADITLAEVLGSLEVGRLVGRYOMRTRTLRGHLAKIYA 60
Qy 61 MHWATDSKLIVSASODGKLIWDTTNTKVAHPLRSSVWMTCAVAPSGNFVACGGIDNM 120
Db 61 MHWATDSKLIVSASODGKLIWDTTNTKVAHPLRSSVWMTCAVAPSGNFVACGGIDNM 120
Qy 121 CSIVNLKSRGNNVKSRELSAHTIGLSCCRFLDDNNNTVSSGDITC----- 166
Db 121 CSIVNLKSRGNNVKSRELSAHTIGLSCCRFLDDNNNTVSSGDITC----- 166
Qy 181 VGHRGDCMSLAVSPDYKLEPISGACDASAKLWDYREGICRQTFGHESDINAICFFNGEA 240
Db 167 -----AKLWDYREGICRQTFGHESDINAICFFNGEA 199
Qy 241 ICGSSDASCRLEPLRADOELTAYSHESICIGTSVAFLSGRLFAGYDDNCNWDSL 300
Db 200 ICHGSSDASCRLEPLRADOELTICFSHESICIGTSVAFLSGRLFAGYDDNCNWDSL 259
Qy 301 KCERGVGVLSGHDNNSVCLGTADGMAVGWSMDFLKWN 340
Db 260 KSERVGLSGLSDNRVSCLGVTADGMAVGWSMDFLKWN 299
RESULT 5
US-08-190-802A-45
; Sequence 45, Application US/08190802A
; Patent No. 5,519,003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33 875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28
; US-08-190-802A-45

Query Match 81.1%; Score 1467; DB 1; Length 341;
Best Local Similarity 79.9%; Pred. No. 1.2e-142;
Matches 270; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

Qy 3 EMEQLKQEAQKKQIADARKACADITLAEVLGSLEVGRLVGRYOMRTRTLRGHLAKIYAH 62
Db 4 EMEALROBEQKQIKNQREKAAADTLMATANPVGRYOMRTRTLRGHLAKIYAH 63
Qy 63 WATDSKLIVSASODGKLIWDTTNTKVAHPLRSSVWMTCAVAPSGNFVACGGIDNMCS 122
Db 64 WASDRNIVSASQDGKLIWDTTNTKVAHPLRSSVWMTCAVAPSGNFVACGGIDNMCS 123
Qy 123 TSLSKSRGNNVKSRELSAHTIGLSCCRFLDDNNNTVSSGDITC----- 182
Db 124 TSLSKSRGNNVKSRELPHTGIGYLSCCRFLDDNNNTVSSGDITC----- 183
Qy 183 HPGDCMSLAVSPDYKLEPISGACDASAKLWDYREGICRQTFGHESDINAICFFNGEAIC 242
Db 184 HPGDCMSLAVSPDYKLEPISGACDASAKLWDYREGICRQTFGHESDINAICFFNGEA 243
Qy 243 TGSDDASCRLEPLRADOELTAYSHESICIGTSVAFLSGRLFAGYDDNCNWDSLKC 302
Db 244 TGSDDASCRLEPLRADOELTAYSHESICIGTSVAFLSGRLFAGYDDNCNWDSLKC 303
Qy 303 ERVGVLSGHDNNSVCLGTADGMAVGWSMDFLKWN 340
Db 304 ERAGVLAGHDNNSVCLGTADGMAVGWSMDFLKWN 341
RESULT 6
US-08-190-802A-40
; Sequence 40, Application US/08190802A
; Patent No. 5,519,003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto

STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, ve
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190, 802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33, 875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0980
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 340 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G- BETA DROSOPH
 US-08-190-802A-40

Query Match 80.3%; Score 145;
 Best Local Similarity 76.5%; Pred. No.:
 Matches 260; Conservative 38; Mismatch
 QY 1 MGEMEOLKQAEEDKKQADARKACADITLAI
 Db 1 MNEELDSLRAEESLKAIRDRDARKACDTSLQP
 QY 61 MHWRATDSKLIVSASQDGKLIVMDTYTINKVHAA
 |||||:|||||:|||||:|||:|||||:|||||:|||||:|||||:
 61 MHWGNDNSRNUVSASQDGKLIVMDSTTNNKVHAA
 Db 121 CSITSLKSREGNPKVSRELASHINGILSCRFELL
 |||||:|||||:|||||:|||:|||||:|||||:|||||:|||||:
 121 CSITNLKTREGNPKVSRELASHINGILSCRFELL
 Db 181 VGHGDCMSLAQSDYKLFISGACDASAKLWDY
 181 LGHGDVMALLSLAPQCKKFVSGACDASKLWDY
 QY 241 ICGSDDASCRFLRLPQDEELTAYSHESITTCG
 |||||:|||||:|||||:|||||:|||:|||||:|||||:
 241 FATGSDDATCRLFDIAROELAMSHDNITCG
 Qy 301 KCERYGVLSQHDNRVSCIGVTAGCMAVTGSMW
 |||||:|||||:|||||:|||||:|||||:
 301 KAERSGLAGHDNRVSCIGVTENGMAVTSW
 Db

RESULT 7
 US-08-190-802A-39
 Sequence 39, Application US/08190802A
 ;
 ; Patient No. 5519003
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Moohly Rosen, Daria
 ; APPLICANT: Ron Dorit
 ; TITLE OF INVENTION: WD - Derived F
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265

, Fig. 23
 2; DB 1;
 4 2e-141
 ches 42

Length	340;	;	Indels	C
QMRTRRTTRGHLF				
QMRTRTTLRGLHAA				
AYAAMSNGFYACAGC				
CAVAPSGSYVACGGC				
DTTCAALWDIETGPOO				
DMSCGIWDIDETGGLD				
TGCHESDINAICFFFFF				
PGHESDINAIVTFFFFF				
RILFAGYDDENCNWNN				
RLLAGYDDNFCNCNT				

; Gaps 0;
KIYA 60
KIYA 60
LDNM 120
LDNM 120
LDNM 120
LDNM 120
KTVF 180
KTVF 180
KVTSF 180
NGEA 240
NGEA 240
NGQA 240
NWDSL 300
NWDSL 300
NWTM 300

ch
I. Similarity
260; Conservv
KOJADARKACDDIV
|| || || |
NQEDRDKACCCDS
DGKLIIWIDSEANV
||||| :|
DGKLIIWIDSEANV
GNYKVSRLESLHTI
---VSRELPGHYY
AVASPDYKLFISGGAA
ISLAPDGRTEFVGAGA
RLFDLDRADQETATTA
||||| :|
RLFDLDRADQETALM
HDHRVSCIGVYADD
||||| :|
HDNRVSCIGVYADD

ovine (2), Fic
re 1419; DB J
3; No. 9-8-e-13
4 mismatches

; Length 3260
; 8: Index
; 33; Index
; LAKIYAMHWATDSI
; ||||| ||||| |||||
; LAKIYAMHWGTDSDS
; ||||| ||||| |||||
; FVAGCGGLDNMCSS
; ||||| ||||| |||||
; FVAGCGGLDNMCSS
; ||||| ||||| |||||
; DGETGQQTIVFGGLDNMCSS
; ||||| ||||| |||||
; DGETGQQTIVFGAGI
; ||||| ||||| |||||
; WAICFPPNGBAIC
; ||||| ||||| |||||
; WAIAFFPNGYAAFT
; ||||| ||||| |||||
; DDFNCNWDSLKIC
; ||||| ||||| |||||
; DDFNCNWDSLKIC
; ||||| ||||| |||||

;:
10; Gaps
ILVNSAS 74
|||||
ILVNSAS 60
|||||
IYIYSLKS R 129
|||||
IYIISLKR 120
|||||
INGDOMS 189
||| |||
ISGDWMS 175
|
IGGSDDAS 249
|||||:
IGGSDDAT 235
SERVGILS 309
:| |||:
RAGVILA 295

APPLICANT: Guegler, Karl J.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032,372
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PR-0478 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX:
 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 395 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB01
 CLONE: 78191
 19-032-372-1

QUERY Match 52.3%; Score 946.5; DB 3;
 best Local Similarity 51.9%; Pred. No. 4; 7e-89;
 matches 177; Conservative 56; Mismatches 103;
 4 MEQLQKEAEOLKKQTADARKACADIDIAELVSGLEVYGRVOMM
 : ||| ||| ||| : | : | : | : | : | : | : | : | : | : |
 54 LASIKSEAESLIGKLEERAKHDLHOAERVEALGQFVMK
 64 ATDSKLVLVSASQDGKLIWDTIYTNTKHAIPLRSSLWMTCAVY
 : | : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
 114 CKDRKIRVISSQDGKVLYWMSFTTNIKEHAVTMCTWMCAYR
 124 YSL--KSREGNVKVRRELSAHGTGJSCCRFLD-DNNIVTSSGG
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 174 YPLTIDKNNENMAKKKSQVAMITNLSACSFNTNSDMQITASG
 181 VGHGTD--CMSLAVSPDYKLFISGACDASAKLWDVREBGTCROT
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 234 HGHGADVCLIDLAPSETGNTFVGSGCDKMMWDMRSQGCVQA
 239 EAICGSDASCRFLRQDQELTASHSIICIGITSAFSL
 : | : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
 294 DAFASGSDDAMCRLYDARREBVAWSKESIIGGASSYDFSL
 299 SLKCERYGVTSVGHDRNVRSCLGTVTADGMAGATVGSWDSFKW
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 354 VLKGSRVSIILGHENRVSTLRVSPDGTAFCSSWSDHTLRW

APPLICANT: Guegler, Karl J.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032,372
 FILING DATE: 08/09/2003
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0478 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 395 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB1
 CLONE: 78191
 9-032-372-1

Query Match 52.3%; Score 946.5; DB 3; Length 395;
 best local similarity 51.9%; Pred. No. 4; 7e-89; Mismatches 177; Conservative 56; Indels 5; Gaps 3; Matches 103;

4 MEQLQEAQELKKQIADARKACADITLAELVSGLEVVGRVQHTRRTRGLAKTYAMHW 63
 54 LASLKSKEASLKGKLEERAKLHDVELHQVAERVEALGQFVWKRTRTLKGHNKVLMDW 113
 64 ATDSKLILVASQDQKLIWDTYTINKVHAIPRLSSWMTCAVAPSGNFWVACGGLDNMC 123
 114 CKPRRIVYSSQDQKVWDFSEFTKHEAVTMCTWNCATAPSGCAIACGGIDNMC 173

124 YSL--KSRREGNVKVSRELSAHTGYLSQRFLD-DNNIVTSSGDTICLWDIETQQKTVF 180
 174 YPLTFDKNEENMAKKKSYAMHTNLVSCSFTNSDMQIATASGDTCLWDVSGQLQSF 233

181 VGRGKD - CMSLAVSPDYKLFITGACDASKLMDVRETCRQFTGHBSDDINACICFFPVG 238
 234 HGHGADVLCQLDLARSETGTNTFVSGGCDDKAMVWDMRSQCVQAFETHEDSINSVRYPSG 293
 239 EAICGSDASCRIFLDRDQELTAYSHESITCGITSVAFSLSGRLIPAGYDFNCNW 298
 294 DAFSSGSDATCRYDLDRADREYATYSKESIIFGASSDTSFSGRLIPAGYNDYTINWD 353
 299 SLKGERVGVLSGHDRNRVSCLGIVADGMAVATGSWDSFLKIKW 339
 354 VLKSRSRVSLFGHNRVSTLRVSPDGTAFCSGSGWDHTLRW 394

RESULT 9
 US-09-190-802A-61
 Sequence 61, Application US/09/032,372
 Patent No. 551903
 GENERAL INFORMATION:
 APPLICANT: Ron Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Delhinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 423 amino acids
 TYPE: amino acid
 TOPOLogy: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: STE4 - YEAST, FIG. 44
 US-08-190-802A-61

Query Match 35.3%; Score 639; DB 1; Length 423;
 best local similarity 36.3%; Pred. No. 2; 1e-57; Mismatches 139; Conservative 74; Indels 124; Matches 139;

3 EMEQLQEAQELKKQIADARKACADITLAELVSGLEVVGRVQHTRRTRGLAKTYAMHW 63
 38 KIEAROESQKOLHAQINTKAKHIIQDASLFLQMKVSLTKRNKLNKPQ 113
 61 MHATDSKLILVASQDQKLIWDTYTINKVHAIPRLSSWMTCAVAPSGNFWVACGGIDNMC 123
 98 FWRMSDKRILVASQDQKLIWDTYTINKVHAIPRLSSWMTCAVAPSGNFWVACGGIDNMC 173
 121 CTSYLSKSREGNVKVSRELSAHTGYLSQRFLD-DNNIVTSSGDTICLWDIETQQKTVF 180
 158 CTYIYR-SKERNVYAQNVNPAFISGKHTCYISDEFDWAHLTASGDMTC 233
 179 VFVGHGDPMSLAVSPDYKLFITGACDASKLMDVRETCRQFTGHBSDDINACICFFPVG 238
 217 EYSDHGLVYALAIPEEPNLNSNTFASCSDGTYIWDSRSRSPSAVQ 293
 233 CFPNGEARLCTGSDDASCRIFLDRADREYATYSKESIIFGASSDTSFSGRLIPAGYNDYTINWD 353
 277 RFFKDGMSIVAGSDNGANNMYDLSRCSIASFTSLFRGYEERTPTPTMM 339
 267 ESTIC-----GTTSVAFSLSGRLIPAGYDFNCNW 394
 337 QIKSTSSSYLDNQGVWSLDFASGRMLMYCITYDGGVWWVWLKGIV

RESULT 10
 US-08-190-802A-27
 Sequence 27, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Behlinder & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REFERENCE NUMBER: 33,875
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: RACK1 Amino Acid Sequence, Fig. 1C
 US-08-190-802A-27

Query Match 16.4%; Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Inends 15; Gaps 5;

Qy 48 RRTLRLGHLLAKIYAHWWATDSKLVLVASQDGKLIWDTYTINKVHAIPRLSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISSPDGQFALSGSMGDTLRLWDLTGTTTTRRFVGHTKDVLVAFF 115
 Qy 108 SGNEVACGGIDNMOSIYSIKSREGNVKVSRELSAHTGYLSCCREL--DDNNIVYSSG-DT 164
 Db 116 DNROIVSGSRDKTILWNL--GVCKTYWQDESHSEWSCVRESPNNSMPITVSCGMNDK 172
 Qy 165 TCAWLWIDTENGQQKIVFVFGTGDMSLAVSPDYKLFISGACDASAKLWVREGTCRQFTG 224
 Db 173 LVKVNWNLANCKLNKLNHIGHTGYLNTVTWSPDGSICASGGKDQAMWLNEGKHLYTDD 232
 Qy 225 HESDINAICFPNGEALCTGSDDASCREFLRA-----DQEITAVSHESITCGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAAT-GPSIKIWLDLEGKILWVDELKOEVISTSSKAEPQCTSLA 290
 Qy 278 FSLSGRGLIFAGYDDFNCCNW 297

RESULT 11
 US-08-190-802A-41
 Sequence 41, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Behlinder & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REFERENCE NUMBER: 33,875
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G-BETA HUMAN, FIG. 24
 US-08-190-802A-41

Query Match 16.4%; Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Inends 15; Gaps 5;

Qy 48 RRTLRLGHLLAKIYAHWWATDSKLVLVASQDGKLIWDTYTINKVHAIPRLSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISSPDGQFALSGSMGDTLRLWDLTGTTTTRRFVGHTKDVLVAFF 115
 Qy 108 SGNEVACGGIDNMOSIYSIKSREGNVKVSRELSAHTGYLSCCREL--DDNNIVYSSG-DT 164
 Db 116 DNROIVSGSRDKTILWNL--GVCKTYWQDESHSEWSCVRESPNNSMPITVSCGMNDK 172
 Qy 165 TCAWLWIDTENGQQKIVFVFGTGDMSLAVSPDYKLFISGACDASAKLWVREGTCRQFTG 224
 Db 173 LVKVNWNLANCKLNKLNHIGHTGYLNTVTWSPDGSICASGGKDQAMWLNEGKHLYTDD 232
 Qy 225 HESDINAICFPNGEALCTGSDDASCREFLRA-----DQEITAVSHESITCGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAAT-GPSIKIWLDLEGKILWVDELKOEVISTSSKAEPQCTSLA 290
 Qy 278 FSLSGRGLIFAGYDDFNCCNW 297

Query Match 16.4%; Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Inends 15; Gaps 5;

Qy 48 RRTLRLGHLLAKIYAHWWATDSKLVLVASQDGKLIWDTYTINKVHAIPRLSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISSPDGQFALSGSMGDTLRLWDLTGTTTTRRFVGHTKDVLVAFF 115
 Qy 108 SGNEVACGGIDNMOSIYSIKSREGNVKVSRELSAHTGYLSCCREL--DDNNIVYSSG-DT 164
 Db 116 DNROIVSGSRDKTILWNL--GVCKTYWQDESHSEWSCVRESPNNSMPITVSCGMNDK 172
 Qy 165 TCAWLWIDTENGQQKIVFVFGTGDMSLAVSPDYKLFISGACDASAKLWVREGTCRQFTG 224
 Db 173 LVKVNWNLANCKLNKLNHIGHTGYLNTVTWSPDGSICASGGKDQAMWLNEGKHLYTDD 232
 Qy 225 HESDINAICFPNGEALCTGSDDASCREFLRA-----DQEITAVSHESITCGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAAT-GPSIKIWLDLEGKILWVDELKOEVISTSSKAEPQCTSLA 290
 Qy 278 FSLSGRGLIFAGYDDFNCCNW 297

Query Match 16.4%; Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Inends 15; Gaps 5;

Qy 48 RRTLRLGHLLAKIYAHWWATDSKLVLVASQDGKLIWDTYTINKVHAIPRLSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISSPDGQFALSGSMGDTLRLWDLTGTTTTRRFVGHTKDVLVAFF 115
 Qy 108 SGNEVACGGIDNMOSIYSIKSREGNVKVSRELSAHTGYLSCCREL--DDNNIVYSSG-DT 164
 Db 116 DNROIVSGSRDKTILWNL--GVCKTYWQDESHSEWSCVRESPNNSMPITVSCGMNDK 172
 Qy 165 TCAWLWIDTENGQQKIVFVFGTGDMSLAVSPDYKLFISGACDASAKLWVREGTCRQFTG 224
 Db 173 LVKVNWNLANCKLNKLNHIGHTGYLNTVTWSPDGSICASGGKDQAMWLNEGKHLYTDD 232
 Qy 225 HESDINAICFPNGEALCTGSDDASCREFLRA-----DQEITAVSHESITCGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAAT-GPSIKIWLDLEGKILWVDELKOEVISTSSKAEPQCTSLA 290
 Qy 278 FSLSGRGLIFAGYDDFNCCNW 297

Query Match 16.4%; Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Inends 15; Gaps 5;

Qy 48 RRTLRLGHLLAKIYAHWWATDSKLVLVASQDGKLIWDTYTINKVHAIPRLSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISSPDGQFALSGSMGDTLRLWDLTGTTTTRRFVGHTKDVLVAFF 115
 Qy 108 SGNEVACGGIDNMOSIYSIKSREGNVKVSRELSAHTGYLSCCREL--DDNNIVYSSG-DT 164
 Db 116 DNROIVSGSRDKTILWNL--GVCKTYWQDESHSEWSCVRESPNNSMPITVSCGMNDK 172
 Qy 165 TCAWLWIDTENGQQKIVFVFGTGDMSLAVSPDYKLFISGACDASAKLWVREGTCRQFTG 224
 Db 173 LVKVNWNLANCKLNKLNHIGHTGYLNTVTWSPDGSICASGGKDQAMWLNEGKHLYTDD 232
 Qy 225 HESDINAICFPNGEALCTGSDDASCREFLRA-----DQEITAVSHESITCGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAAT-GPSIKIWLDLEGKILWVDELKOEVISTSSKAEPQCTSLA 290
 Qy 278 FSLSGRGLIFAGYDDFNCCNW 297

RESULT 12
 US-08-190-802A-47
 ; Sequence 47, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30
 ; US-08-190-802A-47

Query Match 16.4%: Score 297.5; DB 1; Length 317;
 Best Local Similarity 30.8%; Pred. No. 1.7e-22;
 Matches 80; Conservative 46; Mismatches 119; Indels 15; Gaps 6;
 Qy 48 RRTURGHAKTYAMHWATSKLLVYASQDGKLVWWDIYTNTKVAIPRLSSWMTCA-YAPSGNFVA 107
 Db 56 ORAQRGHSHPFDVTTSSDQFALGSMDGTLLWDLTGTTRRFGHTKQVLSVASS 115
 Qy 108 SGNFVACGGDNMCISIYSIKSREGNVKSRELSAHTGVLSCCRFL--DDNNNTVSSG-DT 164
 Db 116 DNROVIVSGSRDKTILKWLWHL--GVCKTYWQDHSHEWNSCVRFPNSNPITVSCWDK 172
 Qy 165 TCAIWLDIETGQQKTVFVGHTGDCMSLAVSPDYKLFTSACADASAKLWDYRESGTCRQFTG 224
 Db 173 LVKVWNLANCKLTNIGHTGYLNTVTVPSPDGSLCAGSGKDQAMLWMDNEGRKHLTYLDG 232
 Qy 225 HESDINATCFFPNEAICGTGSDDASCRLFDR--DOELTAYSHESICGTSVA 277
 Db 233 GDI-INALCFSPRYWILCAAT-GPSIRIWKDLAGKIVDELKOEVINSSKARPPOTSLA 290
 Qy 278 FSLSGRLLFAGYDFNCNW 297
 Db 291 WSADGQTLFAGYDIDNLVRYW 310

RESULT 13
 US-08-190-802A-62
 ; Sequence 62, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 704 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TIF, Fig. 45
 ; US-08-190-802A-62

Query Match 16.3%: Score 295; DB 1; Length 704;
 Best Local Similarity 27.8%; Pred. No. 9.8e-22; Length 704;
 Matches 88; Conservative 51; Mismatches 133; Indels 44; Gaps 9;
 Qy 55 LAKIYAHWATSKLLVYASQDGKLVWWDIYTNTKVAIPRLSSWMTCA-YAPSGNFVA 113
 Db 345 LAKLKAAREAS-KRLASKDQPLPSAVF--YTV-----LNOSHCGVCAEISDDSTMIA 393
 Qy 114 CGGLDNMCISI-----KSRGENVK-----VSREL-SAHTGVL 146
 Db 394 CGFGDSSVRINSLTPANWRILKDAKSIRELDKESADINVRMLDDRSGEVTRSLMHTGPV 453
 Qy 147 SCRFIDDNNTVSSGDTTCALWD-ETGQOKTUVPHGTCDCMSLAVSPDYKLISGCD 205
 Db 454 YRCAPAPEMNLISCSEDSTTRLWSLITWSCVVTYRGHVWVWDYRFPHGYFVSCSYD 513
 Qy 206 ASAKLWDVRESCRCRQFTGHSDDINACCPNGEAICGTGSDDASCRLFDRADOLELTAYS 265
 Db 514 KWARLWATDSNQALRVFGHLSLBCVOFHENSNTVATGSSDRVRLWMDNMTQSQRUMT 573
 Qy 266 -HESIIGITISWAFLSISGRLLFAGDFFRNWVWLSLKCERVGHSQHDMRVCISGVTADG 324
 Db 574 GHKG--SVSLLAFSAGRYLALSAGSVDHNTIILWDLNSLVTUJRTSTVTTFSRD 630
 Qy 325 MAVATGSDSTLKIWN 340
 Db 631 TVLMAAGLDDNNLTW 645

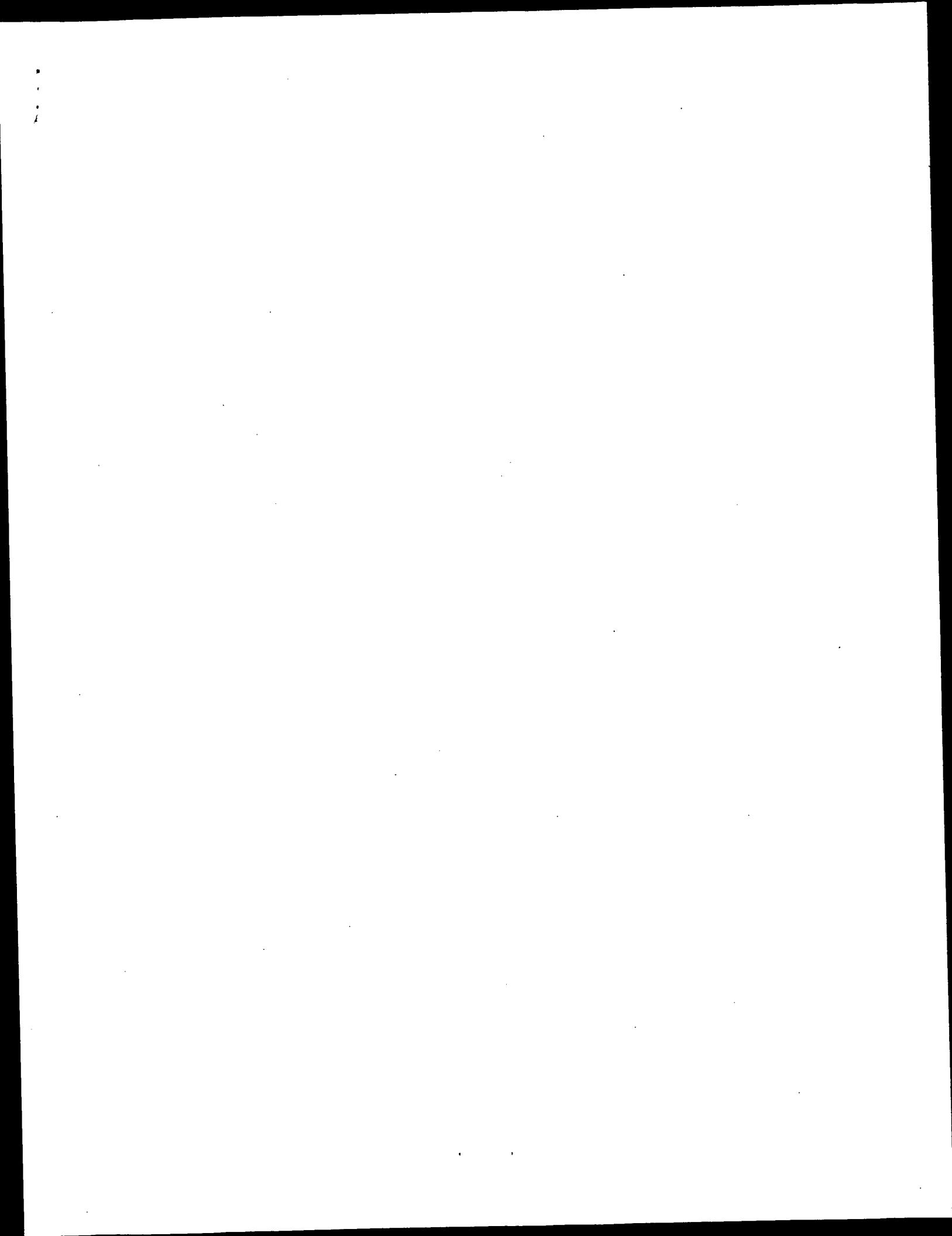
Fri Sep 28 10:45:05 2001

us-09-492-029-3.rai

Page 9

Db 454 YRCAFAPEMNLISCSEDSTIRLWSILTWSCCVVTTYRGHVYPVMDYRFAPHGVYFVSCSYD 513
QY 206 ASAKLNDVRETCROTFTGIESDDINAICFPNGAICIGSDDASCRELDURADQELTAYS 265
Db 514 KTPARLWATDSNQALRVFVGHLSDVDCVOFRPNHNVARTGSSDRVRLNDNMTCQSVRLMT 573
QY 266 -HESTIICGIVNSVAEFLSGRLFAGYDDFCNVWDSLKCERVGVLUSGHDNRVCGLGVADG 324
Db 574 GHKG---SVSSLAFSACGRYLASGSVDHNIIIDLSNGSLVITLRLHTSTVTTFSRDG 630
QY 325 MAVANGSWDSEFLKIN 340
Db 631 TVLAAGLDNNLTWD 646

Search completed: September 28, 2001, 10:28:39
Job time: 30 sec



SQ	SEQUENCE	340 AA;	340	WD AA;	37180 MN;	020A41F754E4B1DA CRC64;
Query Match		100.0%		Score 1809; DB 1;	Length 340;	
Best Local Similarity		100.0%		Pred. No. 2.4e-151;		
Matches	340;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGEQEQLQKEAQEQLKKQIAQDARKACADITIAELVSGLEVGVRMURRTLURGHAKIYA	60			
Db	1	MGEQEQLQKEAQEQLKKQIAQDARKACADITIAELVSGLEVGVRMURRTLURGHAKIYA	60			
QY	61	MHWATSKLLVYASASODGKLIVWPDWYTNTKVKHAPLRSWWMTCAYAPSGNEMVACCGLDNM	120			
Db	61	MHWATSKLLVYASASODGKLIVWPDWYTNTKVKHAPLRSWWMTCAYAPSGNEMVACCGLDNM	120			
QY	121	CSSIKSKRGNVSKVRSLSAHGVLSCREFDNNIVTSSGDTCALNDIEGQQKTVF	180			
Db	121	CSSIKSKRGNVSKVRSLSAHGVLSCREFDNNIVTSSGDTCALNDIEGQQKTVF	180			
QY	181	VGHGDCMSLAVSDYDYLIFSCACDASAKLMDVRGTCRQTFCHESDINA(CFFP)GEA	240			
Db	181	VGHGDCMSLAVSDYDYLIFSCACDASAKLMDVRGTCRQTFCHESDINA(CFFP)GEA	240			
QY	241	ICGSDDASCRFLDRADQELTAYSHESICGTSVAFLSGRLFGYDDENCNWDSL	300			
Db	241	ICGSDDASCRFLDRADQELTAYSHESICGTSVAFLSGRLFGYDDENCNWDSL	300			
QY	301	KCERVGLSLGDNRVSCLGVTADGMAVATGSWDSFLKWN	340			
b	301	KCERVGLSLGDNRVSCLGVTADGMAVATGSWDSFLKWN	340			
RESULT	2					
GB3_MOUSE						
		GB3_MOUSE STANDARD:		PRT;	340 AA.	
		06101;				
		15-JUL-1998 (Rel. 36, Created)				
		30-MAY-2000 (Rel. 39, Last sequence update)				
		GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/(S)/G(R) BETA SUBUNIT 3 (TRANSDUCIN BETA CHAIN 3).				
		GNB3				
Mus musculus (Mouse).						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.						
[1]						
SEQUENCE FROM N.A.						
Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M., Ibu J.J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W., Gibbs R.A., Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.						
[2]						
SEQUENCE OF 199-301 FROM N.A.						
STRAIN=CR-1 / HARLAN; TISSUE=Retina;						
WILLIAMS-97011591; PUBMED=685801;						
G protein gene expression during mouse oocyte growth and maturation, Mol. Reprod. Dev. 44:315-323(1995).						
- - FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPase ACTIVITY. FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA). SIMILARITY: CONTAINS 7 WD REPEATS (TRP ASP DOMAINS).						
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its						
RESULTS	3					
GB3_CANFA						
ID	GB3_CANFA	STANDARD:		PRT;	340 AA.	
AC	P79147;					
DT	01-NOV-1997 (Rel. 35, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DT	15-JUL-1998 (Rel. 36, Last annotation update)					
DE	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/(S)/G(R) BETA SUBUNIT 3 (TRANSDUCIN BETA CHAIN 3).					
DE	GNB3.					
OS	Canis familiaris (Dog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
OX	NBPI_TAXID=9615;					
[1]						

RC STRIAIN-ALASKAN MALAMUTE; "TISSUE"-Retina;
 RX MEDLINE=9740956; PubMed=9266671;
 RA Akhmedov N.B.; Piriev N.I.; Ray K.; Acland G.M.; Aguirre G.D.;
 RA Farber D.B.;
 RT Structure and analysis of the transducin beta3-subunit gene, a
 RT candidate for inherited cone degeneration (cd) in the dog.",
 RL Gene 194:47-56(1997).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U52916; AAC48760.1; -.
 CC
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR01632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPOTEINB.
 DR PRINTS; PRO0320; GPOTEINBREP.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS5024; WD_REPEATS_REGION; 1.
 FT REPEAT 53 WD repeat; Multigene family.
 FT REPEAT 95 WD 1.
 FT REPEAT 141 WD 3.
 FT REPEAT 182 WD 4.
 FT REPEAT 224 WD 5.
 FT REPEAT 268 WD 6.
 FT REPEAT 310 WD 7.
 SQ SEQUENCE 340 AA; 37144 MW; 8E3B5A5238E29C37 CRC64;
 Query Match 97.9%; Score 1771; DB 1; Length 340;
 Best Local Similarity 97.4%; Fred. No. 5.1e-148;
 Matches 331; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Gaps 0;
 OX 1 MGEMQQLQKTAEQOKQKADARKACADTLAELVYGLGVGRYQMRTRTRLRGHAKIYA 60
 Db 1 MGEMQQLQKTAEQOKQKADARKACADTLAELVYGLGVGRYQMRTRTRLRGHAKIYA 60
 QY 61 MHWATDSKLIVSASQDGKLIVWDYTTNKVHAFLRSLSWMTCAYAPSGNFEVACGGIDNM 120
 Db 61 MHWATDSKLIVSASQDGKLIVWDYTTNKVHAFLRSLSWMTCAYAPSGNFEVACGGIDNM 120
 QY 121 CSIVSLSKSEGVNVWSRELSAHTGVLSCRFDDNNNTTSGGTTCAIMDIEFGQKTVF 180
 Db 121 CSIVSLSKSEGVNVWSRELSAHTGVLSCRFDDNNNTTSGGTTCAIMDIEFGQKTVF 180
 QY 181 VGHMGDCMLAVSDEKKERISGACDASKLWDREGTORQTFGESINAQCFPPNEA 240
 Db 181 VGHMGDCMLAVSDEKKERISGACDASKLWDREGTORQTFGESINAQCFPPNEA 240
 QY 241 ICIGSSDDASCRLFDRADQELTAYSHESTICGITSVARSLSGRLLAGYDDFNCFNWDSL 300
 Db 301 KCERVGVTSQHNDNRVSCLGVTAGMMAVATGSMWSEFLKWN 340
 301 KGERVGLSLGHDNRVSCLGVTADGMAMATGSMWSEFLKWN 340
 301 KGERVGLSLGHDNRVSCLGVTADGMAMATGSMWSEFLKWN 340
 RESULT 4
 GBB3_HUMAN ID_GBB3_HUMAN STANDARD; PRT; 340 AA.
 AC P16520;
 DT 01-AUG-1990 (Rel. 15, created)
 DT 01-AUG-1990 (Rel. 15, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
 DE (TRANSDUCIN BETA CHAIN 3).
 GNB3.
 OS Homo sapiens (Human).
 OC Bucephala; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9019801; PubMed=2107550;
 RA Levine M.A.; Simalwood P.M.; Moen P.R. Jr.; Helman L.J.; Ahn T.G.;
 RA Spinos S.; Malley T.; Gibbs R.A.;
 RT "Molecular cloning of beta 3 subunit, a third form of the G protein
 beta-subunit polypeptide.",
 RT Proc. Natl. Acad. Sci. U.S.A. 87:2329-2333(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9630395; PubMed=8723724;
 RA Ansari-Lari M.A.; Muzny D.M.; Lu J.; Lu F.; Lilley C.E.,
 RA Spanos S.; Malley T.; Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 genes at human chromosome 12p13.",
 RT Genome Res. 6:314-326(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Busch S.; Dyrh W.; Siffrert W.;
 DR Submitted (Apr-1997) to the EMBL/Genbank/DDBJ databases.
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M31328; AAC52582.1; -.
 DR EMBL; U47924; AAC51313.1; -.
 DR EMBL; Y12050; CAJ72779.1; -.
 DR EMBL; Y12051; CAJ72779.1; JOINED.
 DR EMBL; Y12052; CAJ72779.1; JOINED.
 DR EMBL; Y12053; CAJ72779.1; JOINED.
 DR EMBL; Y12054; CAJ72779.1; JOINED.
 DR EMBL; Y12055; CAJ72779.1; JOINED.
 DR EMBL; Y12056; CAJ72779.1; JOINED.
 DR EMBL; Y12057; CAJ72779.1; JOINED.
 DR EMBL; Y12058; CAJ72779.1; JOINED.
 DR EMBL; U47930; AAC50468.1; -.
 DR EMBL; A55096; RGHUB3.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR InterPro; IPR00400; WD40; 7.
 DR InterPro; IPR04901; ITBG.
 DR MIM; 139130; -.
 DR InterPro; IPR001680; -.
 DR InterPro; IPR00400; WD40; 7.
 DR PRINTS; PR00319; GPOTEINB.
 DR PRINTS; PR00320; GPOTEINBREP.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 CC Transducer; Repeat; WD repeat; Multigene family.

FT	REPEAT	53	83	WD 1.
FT	REPEAT	95	125	WD 2.
FT	REPEAT	141	170	WD 3.
FT	REPEAT	182	212	WD 4.
FT	REPEAT	224	254	WD 5.
FT	REPEAT	268	298	WD 6.
FT	REPEAT	310	340	WD 7.
SO	SEQUENCE	340 AA;	37221 MW;	896E706A61B8B74F CRC64;
Query	Match	97.4 %;	Score 1762;	DB 1; Length 340;
Best Local Similarity		97.5 %;	Pred. No. 3. 1e-17;	
Matches		328;	Conservative	8; Mismatches
QY	1	MGEOMEOLKQAEQLKKQIADARKACADITLAEVLGLEYWGRVQMRTRTLRGLAKIYA	60	
Db	1	MGEMEOLRQEAQQLKQIADARKACADITLAEVLGLEYWGRVQMRTRTLRGLAKIYA	60	
QY	61	MHWATDSKLIVSASODGKLYIWDTYTNNKHAIPRSSWMTCAVAPSGNFVAGGLDNM	120	
QY	61	CSIYNIKSRSCKNVYVSELRAHTGYSCLCCFLDDNTIVTSSGDTCALMDIEGQKTV	120	
Db	61	MHWATDSKLIVSASODGKLYIWDTYTNNKHAIPRSSWMTCAVAPSGNFVAGGLDNM	120	
QY	121	VGHGDGMSLAQSPDVKLFTSGACASAKLWDVREGTCRQFTGHESDINACIFPPNGEA	240	
Db	181	VGHGDGMSLAQSPDNLFTSGACASAKLWDVREGTCRQFTGHESDINACIFPPNGEA	240	
QY	241	ICTGSIDASCRFLDRLADQETAYSHESITCGITSVAFSGRLFLAGIDDFNCNWDSI	300	
Db	241	ICTGSIDASCRFLDRLADQETAYSHESITCGITSVAFSGRLFLAGIDDFNCNWDSI	300	
QY	301	KCERVGVLGSDHNRVSLGIVYVADGMVATWSWDSLKWN 340		
Db	301	KSERVGILGSDHNRVSLGIVYVADGMVATWSWDSLKWN 340		
RESULT	5			
ID	GB1_HUMAN	STANDARD;	PRT;	340 AA.
AC	PO4901; P04697;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1 (TRANSDUCIN BETA CHAIN 1).			
GN	GB1L			
OS	Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NEBI_TAXID-9606, 10090, 9913, 9615;			
RN	1)			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human; TISSUE=Liver;			
RX	MEDLINE=87070912; PubMed=3095147;			
RA	Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;			
RT	"Beta subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical.";			
RT	FEBS Lett. 207:187-192(1986).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	SPECIES=Mouse; TISSUE=Adrenal gland;			
RC	Medline:86177563; PubMed=3083416;			
RC	Fong H.K.W., Hurley J.B., Hopkins R.S., Maake-Lye R., Johnson M.S., Doolittle R.F., Simon M.I.;			
RA	Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Bovine;			
RX	Medline:86177563; PubMed=3083416;			
RA	Fong H.K.W., Hurley J.B., Hopkins R.S., Maake-Lye R., Johnson M.S., Doolittle R.F., Simon M.I.;			
RT	"Repetitive segmental structure of the transducin beta subunit: homology with the CDC4 gene and identification of related mRNAs".			
RT	Proc. Natl. Acad. Sci. U.S.A. 83:2162-2166(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Bovine;			
RX	MEDLINE=86030675; PubMed=2414128;			
RA	Sugimoto K., Nakada T., Takahashi H., Noda M., Minamino N., Ra Kangawa K., Matsuo H., Hirase T., Inayama S., Numa S.;			
RT	"Primary structure of the beta-subunit of bovine transducin deduced from the cDNA sequence".			
RT	J. Biol. Chem. 260:235-240(1985).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=C. familiaris;			
RX	MEDLINE=9745667; PubMed=9300552;			
RA	Kylma T., Paulin L., Hurwitz M.Y., Hurwitz R.L., Kommonen B.;			
RT	"Cloning of the cDNA encoding rod photoreceptor GMP-phosphodiesterase alpha and gamma subunits from the retinal degenerate Labrador retriever dog".			
RT	Res. Vet. Sci. 62:293-296(1997).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.			
RX	MEDLINE=9745667; PubMed=9300552;			
RT	"The structure of the G-protein heterotrimer Gi alpha 1 beta 1 gamma 2.".			
RL	Cell 83:1047-1058(1995).			
RN	[7]			
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.			
RX	MEDLINE=96149354; PubMed=8521505;			
RA	Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A., Gilman A.G., Sprang S.R.;			
RT	"The structure of the G-protein heterotrimer Gi alpha 1 beta 1 gamma 2.".			
RL	Science 267:1047-1058(1995).			
RN	Nature 379:369-374(1996).			
RN	[8]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.			
RX	MEDLINE=98416596; PubMed=9739091;			
RA	Lew A., Ho Y.K., Blundell T., Bax B.;			
RT	"Phosducin induces a structural change in transducin beta gamma.";			
CC	Structure 6:1007-1019(1998).			
-	FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.			
CC	- - SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).			
CC	-- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.issb-sib.ch/announce/ or send an email to license@issb-sib.ch).			
CC	-----			
DR	EMBL; X04526; CAA28207.1; -			
DR	EMBL; U29055; AAC52905.1; -			
DR	EMBL; X03073; CAA26875.1; -			
DR	EMBL; Z75134; CAA9946.1; -			
DR	PIR; A24893; RGUBL;			
DR	PIR; A24225; RGBOBL;			
DR	PDB; 1GG2; 12-FEB-97;			
DR	PDB; 1GP2; 12-FEB-97;			
DR	PDB; 1TBG; 01-APR-97;			
DR	PDB; 1AQI; 16-FEB-99;			
DR	PDB; 1B9X; 23-FEB-99;			
DR	PDB; 1BY9; 23-FEB-99;			
DR	MMDB; 139380; -			

DR MGD; MGI:95781; Gbhl.
 DR InterPro; IPR001632; -.
 DR Pfam; PF00400; WD001; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 KW Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V->L (IN REF. 4).
 SQ SEQUENCE 340 AA: 37377 MW: 896CB3D2B2686598 CRC64;
 DR RSLNKLKREGNVRSRELAGHTGYLSCRFDDNQVITSGTTCAIWDIEGQQTTF 180
 DR HSSP; X86969; CAA60332.1; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pram; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37330 MW: DE036FF602D6A9 CRC64;
 DR RSLNKLKREGNVRSRELAGHTGYLSCRFDDNQVITSGTTCAIWDIEGQQTTF 180
 DR HSSP; X86969; CAA60332.1; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pram; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37330 MW: DE036FF602D6A9 CRC64;
 DR RSLNKLKREGNVRSRELAGHTGYLSCRFDDNQVITSGTTCAIWDIEGQQTTF 180
 DR HSSP; X86969; CAA60332.1; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pram; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37330 MW: DE036FF602D6A9 CRC64;
 DR RSLNKLKREGNVRSRELAGHTGYLSCRFDDNQVITSGTTCAIWDIEGQQTTF 180
 DR HSSP; X86969; CAA60332.1; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pram; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37330 MW: DE036FF602D6A9 CRC64;

Query Match	82.6%	Score 1495; DB 1; Length 340;
Best Local Similarity	79.4%	Pred. No. 8.1e-124; Mismatches 31; Indels 0; Gaps 0;
Matches 270; Conservative	31;	Mismatches 39; Indels 0; Gaps 0;
Drift 270;		
PRINTS; PRO319; GPROTEINB.		
DR PRINTS; PRO320; GPROTEINBRPT;		
DR PROSITE; PS00618; WD_REPEATS 1; 3.		
DR PROSITE; PS50022; WD_REPEATS 2; 6.		
DR PROSITE; PS5024; WD_REPEATS_REGION 1.		
KW Transducer; Repeat; WD repeat; Multigene family.		
DR REPEAT 53 83		
FT REPEAT 95 125	WD 1.	
FT REPEAT 141 170	WD 2.	
FT REPEAT 182 212	WD 3.	
FT REPEAT 224 254	WD 4.	
FT REPEAT 268 298	WD 5.	
FT REPEAT 310 340	WD 6.	
SQ SEQUENCE 340 AA; 3754 MW; B21EB29BA862B1E CRC64;		
RESULT 12		
181 VGHGDCMSLAVSDYKIFISGACDASAKLWDREGTCROTGFHESDINACFFNGEA 240		
181 AGHSQDVMSLISLADPGRFVSGCDAKSILKWLWRESCMRCQFIGHESDINAVFFFNGYA 240		
241 ICTGSDDASCRLFDLRADQELTAYSHESITCCITSVAFSLSGRLLAGYDFNCNWDSL 300		
241 FTGSDDATCRFLDRLRADQELTAYSHESITCCITSVAFSLSGRLLAGYDFNCNWDSL 300		
301 KCERGVLSGHDNRVSCIGVADGMATGWSDSFLKINW 340		
301 KCERGVLSGHDNRVSCIGVADGMATGWSDSFLKINW 340		
301 KGDRAGVLAGHNDNRVSCIGVTDGMATGWSDSFLKINW 340		
MUS musculus (Mouse).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NBII_TAXID=10090;		
{1}		
SEQUENCE FROM N.A.		
MLN1543505; MEDLINE=92181467; PubMed=1543505; von Weizsaecker E.; Stratmann M.P.; Simon M.I.; "Diversity among the beta subunits of heterotrimeric GTP-binding proteins: characterization of a novel beta-subunit cDNA.", P29387; 01-DEC-1992 (Rel. 24, Created) 183-35-35(1992). -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.		
-I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).		
-I- SIMILARITY: CONTAINS 7 WO REPEATS (TRP-ASP DOMAINS).		
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
RESULT 13		
GBB_LYMNST		
ID GBB_LYMNST STANDARD; PRT; 341 AA.		
AC 008706; DT 01-OCT-1996 (Rel. 34, Created)		
DT 01-OCT-1996 (Rel. 34, Last sequence update)		
DT 15-JUL-1998 (Rel. 35, Last annotation update)		
DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.		
OS Lymnaea stagnalis (Great pond snail).		
OC Lymnacidae; Lymnaea.		
OX NCBI_TaxID=6523;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC TISSUE-CNS;		
RX MEDLINE=94242793; PubMed=7514444; Knoell J.C., Rovers E., van Kesteren E.R.J., Vreudenberg H., van Heerikhuizen H.;		
RA "A G-protein beta subunit that is expressed in the central nervous system of the mollusc Lymnaea stagnalis identified through cDNA cloning.", Biophys. Acta 1222-129-133(1994).		
EMBL; S86124; AAB21609.1; -.		
EMBL; M82286; AAA37756.1; -.		
EMBL; M62658; AAA37664.1; -.		
PIR: JS0069; RGMS1641; -.		
HSSP; P04901; ITBG.		

SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GIPAS ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.

- - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC ---

CC DR EMBL; Z23105; CAA80652.1; -.

CC DR HSSP; P04901; IGP2.

CC DR InterPro; IPR01632; -.

CC DR InterPro; IPR001680; -.

CC DR Pfam; PF00400; WD40; -.

CC DR PRINTS; PR00319; GPROTEINB.

CC DR PROSITE; PS00678; WD_REPEATS_1; 2.

CC DR PROSITE; PS5082; WD_REPEATS_2; 5.

CC DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

CC KW transducer; Repeat; WD repeat.

CC FT REPEAT 54 84 WD 1.

CC FT REPEAT 96 126 WD 2.

CC FT REPEAT 142 171 WD 3.

CC FT REPEAT 183 213 WD 4.

CC FT REPEAT 225 255 WD 5.

CC FT REPEAT 269 299 WD 6.

CC FT REPEAT 311 341 WD 7.

CC SQ SEQUENCE 341 AA: 37520 MW: 442662588387592E CRC64;

Query Match 81 9%; Score 1482; DB 1; Length 341; Best Local Similarity 80.2%; Pred. No. 1.e-122; Matches 271; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

CC OY 3 EMEOLQKEAEQLKKQIADARKACADITLAELVSLLEVGRVQMRRTURGHAKIYAH 62

CC ::| :|| | || | || | :|| | :|| | || | || | || | || | || | || | || | || |

CC Db 4 DLEALRQEHTOLKQIREARAKAAGDTTLAQACSGVEAVORIOMRTTRURGHAKIYAH 63

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC OY 63 WATDSKLVLVASQDGKLIWDTYTINKVHAIPRLPSSWMTCAVAPSGNFWACGGLDNMCS 122

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 64 WASDRNLNVASQDGKLIWDTYTINKVHAIPRLPSSWMTCAVAPSGNFWACGGLDNMCS 123

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC OY 123 IYSLSREGNKVSRBLSAHNGTSCCRFLDDNNITVSSGDTGALWDIETGQOKTVF 182

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 124 IYSLKTRREGNVRVSRBLPQHGTGILSCRFIDNSITVSSGMSCALWDIETGQOTTSFG 183

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Oy 183 HTGDCMSLAVSPDYLKFISACDASAKLWVREGTCRQRTFGHESIDINAICFFPNEAIC 242

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 184 HNGDVMSLSTSPDFFRTFVSGACDASAKLWVRDGMCKQTFSGHESIDINAITYFNGHAF 243

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Oy 243 TGSDDASCRFLDRQDQELTAYSHSITIGCTSVAFSLSGRLLAGYDFPNCNTWDSLIC 302

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 244 TGSDDATCRLFIDRAQDQEGMYSHDNITCIGITSVAFSKSGRLLGRYDFFNCNVWDLHQ 303

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Oy 303 ERVGVLISGGHNRVSCIGTGTAGMAYATGSMDSFLKTN 340

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 304 ETHGVLAGHNDNRVSCIGTGTAGMAYATGSMDSFLKTN 341

CC ---

CC RESULT 14

CC GBL_HOMAM STANDARD; PRT; 340 AA.

CC AC 045040;

CC ID GBL_HOMAM

CC DT 15-DEC-1998 (Rel. 37, Created)

CC DT 15-DEC-1998 (Rel. 37, Last sequence update)

CC DT 30-MAY-2000 (Rel. 39, Last annotation update)

CC DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 1 (TRANSDUCIN BETA CHAIN 1).

GN GBeta1.

OS Homarus americanus (American lobster).

OC Arthropoda; Crustacea; Malacostraca; Eukaryota; Metazoa; Arthropoda; Crustacea; Eumalacostraca; Eucarida; Decapoda; Plecoyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.

OX NCBI_TAXID=6706;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98410740; PubMed=9740024;

RA Xu F., Hollins B., Landers T.M., McClintock T.S.;

RT "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in olfactory receptor neuron dendrites and brain neuropil.";

RT J. Neurobiol. 36:525-536(1998).

CC J. NEUROBIOLOGY 36:525-536(1998).

CC ---

CC - - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

CC DR EMBL; AFO44735; AAC02998.1; -.

CC DR PRINTS; PR00319; GPROTEINB.

CC DR PROSITE; PS00678; WD_REPEATS_1; 3.

CC DR PROSITE; PS50082; WD_REPEATS_2; 6.

CC DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

CC DR REPEATER; WD_REPEATS; Multigene family.

CC FT REPEAT 53 83 WD 1.

CC FT REPEAT 95 125 WD 2.

CC FT REPEAT 141 170 WD 3.

CC FT REPEAT 182 212 WD 4.

CC FT REPEAT 224 254 WD 5.

CC FT REPEAT 268 298 WD 6.

CC FT REPEAT 310 340 WD 7.

CC SQ SEQUENCE 340 AA: 37409 MW: 3483245F9291D82E CRC64;

Query Match 81.6%; Score 1477; DB 1; Length 340; Best Local Similarity 78.2%; Pred. No. 3.e-122; Matches 266; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

CC Oy 1 MGEMEQLKEAEQLKKQIADARKACADITLAELVSLLEVGRVQMRRTURGHAKIYA 60

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 1 MNDSLSRQEARIKNTTARDARNALDPTVATGMPDGTOMRURGHAKIYA 60

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Oy 61 MHWTDSKLVLVASQDGKLIWDTYTINKVHAIPRLPSSWMTCAVAPSGNFWACGGLDNM 120

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 61 MHWGDSRNLNVASQDGKLIWMDSYTINKVHAIPRLPSSWMTCAVAPSGNFWACGGLDN 120

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Oy 121 CSISLSREGNKVSRBLSAHNGTSCCRFLDDNNITVSSGDTGALWDIETGQOKTVF 180

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 121 CSISLKTRREGNVRVSRBLPQHGTGILSCRFIDNSITVSSGMSCALWDIETGQCTQF 180

CC Oy 181 VGHGDCMSLAVSPDYLKFISACDASAKLWVREGTCRQRTFGHESIDINAICFFPNEA 240

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 181 TGHCDMSLISLSPMRITSGACDASAKLWVRDGMQCFPTFGHESIDINAICFFPNEA 240

CC Oy 241 ICTGSDASCRFLDRQDQELTAYSHSITIGCTSVAFSLSGRLLAGYDFPNCNTWDSL 300

CC ::| :|| | || | || | || | || | || | || | || | || | || | || | || | || |

CC Db 241 PATGSDATCRLFIDRAQDQEGMYSHDNITCIGITSVAFSKSGKLLAGYDFPNCNVWDMS 300

QY 301 KCFERVGVLSGIDNRVSCLGVTADGMAVATGSWDSPFLKINN 340
 QY : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 301 RTERAGVLAGHDNRSCLGVTEGDGHAVATGSWDSPFLKINN 340

RESULT 15
 GBB2_BOVIN STANDARD PRT; 326 AA.
 AC P11017;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCTIN BETA CHAIN 2). (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
 GN GNB2.
 OS Bos tauris (Bovine).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TAXID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W.; Amatruda T.T.; Birren B.W.; Simon M.I.;
 RT "Distinct forms of the beta subunit of GTP-binding regulatory
 proteins identified by molecular cloning";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 [2]
 RP SEQUENCE OF 88-302 FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B.; Gilman A.G.; Robishaw J.D.;
 RT "A second form of the beta subunit of signal-transducing G proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION
 -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions is allowed as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M16480; AAA30553.1; --.
 CC DR M3431; AAA62717.1; --.
 CC DR EMBL; M16539; AAA0552.1; --.
 CC DR PIR; A26617; RGBOB2.
 CC DR HSSP; P04901; IGP2.
 CC DR InterPro; IPR01680; --.
 CC DR Pfam; PF00400; WD40; --.
 CC DR PROSITE; PS00678; WD_REPEATS_1; 3.
 CC DR PROSITE; PS50082; WD_REPEATS_2; 6.
 CC DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 CC KW Transducer; Repeat; WD repeat; Multigene family.
 FT NON_TER 1
 FT REPEAT 39
 FT REPEAT 81 111 WD 1.
 FT REPEAT 127 156 WD 2.
 FT REPEAT 168 198 WD 4.
 FT REPEAT 210 240 WD 5.
 FT REPEAT 254 284 WD 6.
 FT REPEAT 296 326 WD 7.
 FT CONFLICT 271 271 L->V (IN REF. 2).
 SQ SEQUENCE 326 AA; 35645 MW; EEB90EFBC51B23 CRC64;

Query Match

81.1%; Score 1467; DB 1; Length 326;

Best Local Similarity 81.0%; Pred. No. 2.e-121;
 Matches 264; Conservative 29; Mismatches 33; Indels 0; Gaps 0;
 QY 15 RKRQIADARKACADITLAELVGLEUVGRYQMRRTLRHLAKIYAHMWATSKLIVAS 74
 Db 1 RNQIRDARKACGDSITQTAGLDPVGRTRRLGHHLAKIYAHMGTDLSLIVAS 60
 QY 75 QDGKLIVWDPYTNTKVHAIPLRSWWMTCAYAPSGNIVACGGLDNMCSTISLKSREGNK 134
 Db 61 QDGKLIIWDSYTNNKVAHPLRSSWMMTCAYAPSGNIVACGGLDNMCSTISLKSREGNK 120
 QY 195 DYKLFISGACDASAKLWVREGTCROTFTGHESDHINACICFPNGAICGSDDDASCREFD 254
 Db 181 DGRPFVSGACDASIKLWVRODSMRCPTFIGEHDINAVAFFPNGAFTGSDATCRLFD 240
 QY 255 LRADQELTAYSHESLICGITSWAFLSGRLLFAGYIDENCNWWSLKCERYGVLSGHON 314
 Db 241 LRADQELLYMSHDNIGITSWAFLSRSGRLLLAGYDDFNINIDAMKGDRAGYVLAGHON 300
 QY 315 VSCLGVIIDGMAVATGSWDSPFLKINN 340
 Db 301 VSCLGVIIDGMAVATGSWDSPFLKINN 326

Search completed: September 28, 2001, 10:34:28
 Job time: 203 sec

Fri Sep 28 10:45:09 2001

us-09-492-029-3.rsp

Fri Sep 28 10:45:10 2001

GanCore - version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:25 ; Search time 38.04 seconds
 (without alignments)
 1182.537 Million cell updates/sec

Title: US-09-492-029-3
 Perfect score: 1809
 Sequence: IKGEMEIQKQAEQQIKQIAD. TADGMAVATIGSWSDSLKINN 340

Scoring table: Biosum62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

20	637	35.2	371	5	Qxavvo	061621 mus musculus t
21	601	33.2	123	11	040456 nicotiana t	09xbdb amyclatrops
22	592.5	32.8	240	10	040456	093445 hom sapien
23	313	17.3	1241	2	09xrb8	093445 streptomyce
24	312	17.2	522	4	043445	091xxg streptomyce
25	310	17.1	1049	2	09zem4	076734 dictyostelia
26	310	17.1	09kx9	1676	09vrx2	09vrx2 hom sapien
27	309	17.1	579	5	076734	09xy00 arabidopsis
28	308.5	17.1	485	4	09nw2	043604 homo sapien
29	308	17.0	333	10	09sy00	074055 schizosacch
30	308	17.0	520	4	043664	043177 homo sapien
31	305	16.9	502	3	074855	09fl1x9 arabidopsis
32	305	16.9	521	4	043172	014432 schizosacch
33	299	16.5	473	10	09t1x9	09uub8 schizosacch
34	295.5	16.3	561	3	014432	09nw7 hom sapien
35	295	16.3	586	3	09uub8	093531 xenopus lae
36	295	16.3	334	4	09nw7	096653 trypanosoma
37	291.5	16.1	476	13	09531	09w711 xenopus lae
38	288.5	15.9	318	5	096653	09vpr4 drosophila
39	286.5	15.8	317	13	09w711	09vvi0 drosophila
40	285.5	15.8	481	5	09vpr4	04083 caenorhabdi
41	284	15.7	553	5	09vwio	09vu65 drosophila
42	284	15.7	587	5	044083	09in19 arabidopsis
43	283.5	15.6	391	5	09vu65	096995 drosophila
44	282.5	15.6	613	10	09fn19	
45	281.5	15.6	480	5	096995	

```

database : SPTRMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mic:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rat:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

No.	Score	Query	Length	DB	ID	Description
1	1670	92.3	340	13	Q9PRG9	Q9dfg9 ambystoma t-
2	1570	86.8	340	13	Q9DBH0	Q9fbh0 ambystoma t-
3	1558	86.1	340	11	Q9QW68	Q9gw68 rattus norv-
4	1506	83.3	340	4	Q9HAV0	Q9hav0 homo sapien
5	1496	82.7	340	11	Q9JHX8	Q9jhx8 mus musculus
6	1253	69.3	352	3	Q93887	Q93887 cryptococcu
7	1225	67.7	347	3	Q9HFS3	Q9hf3 pneumocysti
8	1215	67.2	352	3	Q74214	Q74214 emericella
9	957.5	52.9	358	5	Q9W3J1	Q9w3j1 drosophila
10	946	52.3	395	4	Q9HAU9	Q9hau9 homo sapien
11	830	45.9	346	5	Q9NFZ1	Q9nfz1 calliphora
12	826.5	45.7	377	10	Q9XFK0	Q9xfk0 pilum sativu
13	823.5	45.5	377	10	Q9SW94	Q9sw94 pisum sativu
14	823	45.5	346	5	Q9VW29	Q9vw29 drosophila
15	811	44.8	377	10	Q9FV61	Q9fv61 nicotiana t-
16	794	43.9	380	10	Q64944	Q64944 arena fattua
17	739.5	40.9	283	4	Q9FT3	Q9ft3 homo sapien
18	696.5	38.5	436	5	Q9Y7B8	Q9y7b8 kluyveromyces
19	689	38.1	186	5	Q45041	Q45041 homarus aene

SQ	SEQUENCE	340 AA;	37567 MW;	EDF005155A1EDC89 CRC64;
Query Match	83.3%	Score 1506; DB 4; Length 340;		
Best Local Similarity	79.7%	Pred. No. 3. 5e-130;		
Matches	271;	Conservative 35; Mismatches 34; Indels 0; Gaps 0;		
Qy	1	MGEMEQLKQEAQQLQIAQADITLAEVLSSLEVGRVOMTRRTRGHAKIYA	60	
Db	1	MSELEQURQEAEQLRNOIQDARKACNADITLQITSNMSDVGRQIOMTRRTRGHAKIYA	60	
Qy	61	MHWATPSKLVYASASOPGKLWYDTYTINVKHAIPRLSSWMTAYAPSGLNVAACGGDNM	120	
Db	61	MHWGYPSRLVYASASOPGKLWYDTYTINVKHAIPRLSSWMTAYAPSGLNVAACGGDNM	120	
Qy	121	CSIYSKSREGNVKVSRELSAHTGYLSCRCRFLDDNNIVTSSGDTICALWDIETGQKTV	180	
Db	121	CSIYNLKTRGVNRVRELPGTYLSCRCRFLDDSQVTTSGDTICALWDIETGQKTV	180	
Qy	181	VIGHTGDMSLASPDOKLFLISGACDASAKLMDVREGTQFTGHESDINAICFFNGEA	240	
Db	181	TCHSGDMSLSPDLKTFVSGACDASAKLMDVREGTQFTGHESDINAICFFNGEA	240	
Qy	241	ICTGSDASCRFLDRADQELTAYSHESICIGTTSVAFSLSGRLLPAGYDFNCNWDSL	300	
Db	241	FATGSDATCRFLDRADQELLYSHDNTICGITSVAFSKSGRLLLAGYDDFCNCNWDSL	300	
Qy	301	KCERVGVLSGHDNRVSVCLGIVTAGMAVATGSNSDFELKIWN	340	
Db	301	KGGRSGVLAGHDNRVSVCLGIVTAGMAVATGSNSDFELKIWN	340	
RESULT	5			
09JHXB				
ID	09JHXB	PRELIMINARY;	PRT;	340 AA.
AC	09JHXB;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-MAR-2001 (TREMBLrel. 15, Last sequence update)			
DE	G-PROTEIN BETA-4 SUBUNIT.			
OS	musculus (Mouse)			
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
OX	NCBI_TAXID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
09JHXB				
ID	09JHXB	PRELIMINARY;	PRT;	352 AA.
AC	09JHXB;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	G-PROTEIN BETA SUBUNIT GPB1.			
GN	GPB1.			
OS	Cryptococcus neoformans (Filobasidiella neoformans).			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;			
OC	Tremellaceae; Filobasidiella.			
OX	NCBI_TAXID=5207;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
09JHXB				
RC	STRAINH99;			
RA	Wang P., Perfect J.R., Heitman J.;			
RT	"The G-protein beta subunit GPB1 is required for mating in Cryptococcus neoformans and functions in a pathway distinct from the alpha subunit GPa1."			
RT	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AF091120; AAD05396.1; -.			
DR	HSSP; P04901; ITBG.			
DR	InterPro; IPR005632; -.			
DR	InterPro; IPR001680; -.			
DR	Pfam; PF00400; WD40; 7.			
DR	PRINTS; PR00319; GPROTEINB.			
DR	PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.			
DR	SMART; SM00320; WD40; 1.			
DR	Repeat; WD repeat.			
KW	SEQUENCE WD 352 AA; 37904 MW; 36CF4F16AA2C6AB5 CRC64;			
SQ				
Query Match	69.3%	Score 1253; DB 3; Length 352;		
Best Local Similarity	65.7%	Pred. No. 6. 1e-107;		
Matches	224;	Conservative 56; Mismatches 53; Indels 8; Gaps 0;		
Qy	8	KQEAEQTKQIADARKACADITLAEVLSSLEVGRVOMTRRTRGHAKIYA	67	
Db	12	RREADGKDKLRAARDOTADITSLRAMADTTPPLPRITKARRTLKHAKIYAHADT	71	
Qy	68	KLIVSSQDGKIJWVWYTTNKHAIPRLSSWMTAYAPSGLNVAACGGDNMCSYSIK	127	
Db	72	RHVVASQDGKIJWVWYTTNKHAIPRLSSWMTAYAPSGLNVAACGGDNMCSYSIK	131	
Qy	128	-----SREGNVKVSRELSAHTGYLSCRCRFLDDNNIVTSSGDTICALWDIETGQKTV	179	
Db	132	GAGPGAPGAPGQKYARELHLASGSLCCRFINDQIVVSSGDMCMLOEGRTME	191	
Qy	180	FVGTGDMCLAVSPDYKLTSGACIASAKLMDVDRGTCRQFTGHESDINAICFFNGE	239	
Db	192	FADHTGDVMCLSLAPANLFLVSGACDATAKWDIPTGKAVOTFGESDINAQVFPPNGD	251	
Qy	240	AICTGSDASCRFLDRADQELTAYSHESICIGTTSVAFSLSGRLLPAGYDFNCNWDS	299	

Fri Sep 28 10:45:10 2001

QY 62 HWATDSKLLVSAQDGKLIWDTYTNTKHAIRPLRSSWMTCAYAPSGNFVACGGIDNMC 121
| :
Db 72 DNTPEKRARRIVASQDGKLIWDTYTNTKHAIRPLRSSWMTCAYAPSGNFVACGGIDNSVC 131
| :
QY 122 SYSLKS---RBGNVKVSRLELSAHTGYLSCCREL---DDNNIVTSSGDTTCALWDIENGQQ 176
| :
Db 132 SIFNLNSPIDKDGHNHVSRLMSGHGKVSSCQVFDDETHLTTSGGDOTCVLWDITGLR 191
| :
QY 177 KTVF----VGTDGCMSLAV-SPDYKLFTSGACDASAKLWDYREGI-CROOPTGHESDI 229
| :
Db 192 TSVRGERFQSGHTADKVSVSISSSNPRLVSGSDTTAGIWDTRVASRAQRTFYGHGCV 251
| :
QY 230 NAICFFPGEACTGSDASCRFLDLRADQELTAVSH--ESTICGITSVATISGRILF 286
| :
Db 252 NTVPKSPDONREGTGSENGTCALDIRGHOLQVYQPHGDIPFHVTMSAFSTSGRILF 311
| :
QY 287 AGYDDFNCCNWMDSLKLCERY---GVLSGHDNRVSCIGVTAADMAYATGSWDFEJKIW 339
| :
Db 312 VGYNSNGDCYVWDTLAKVVLNLGGVONSHEGRISCLGLSADGSALCTGSWDTNLKIKW 368

Search completed: September 28, 2001, 10:34:06
Job time: 281 sec

C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C;Accession: A35096
 R;Devine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2329-2333, 1990
 A;Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-subunit
 A;Accession: A35096; MUID:90192801
 A;Molecule type: mRNA
 A;Residues: 1-340 <LEV>
 A;Cross-references: GDB:GNB3
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay signals. The beta and gamma chains, required for GTPase activity, appear to be common to all G-proteins. It is specific for each type of G protein.
 C;Comment: In mammals, four distinct types of beta chains have been found.
 C;Genetics:
 A;Gene: GDB:GNB3
 A;Cross-references: GDB:120005; OMIM:139130
 A;Map Position: 12p13-12p13
 C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology <WD3>
 C;Keywords: GTP binding; heterotrimer; signal transduction
 F;51-84/Domain: WD repeat homology <WD1>
 F;88-126/Domain: WD repeat homology <WD2>
 F;139-171/Domain: WD repeat homology <WD3>
 F;210-213/Domain: WD repeat homology <WD4>
 F;222-255/Domain: WD repeat homology <WD5>
 F;263-299/Domain: WD repeat homology <WD6>
 F;308-340/Domain: WD repeat homology <WD7>
 Query Match .97.4%; Score 1762; DB 1; length 340;
 Best Local Similarity 96.5%; Pred. No. 1; e-138; Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGEMEQOLQEAEGLKKQDADARKACADITLABLEVSLGEVGRVQMRTRRLGHAKIYA 60
 Db 1 MGEMEQOLQEAEGLKKQDADARKACADITLABLEVSLGEVGRVQMRTRRLGHAKIYA 60
 QY 61 MHWATDSKLLVVASQDGKLIVWDTYTINVKHAIPRSSLWMTCAVAPSGNFVACGGIDM 120
 Db 61 MHWATDSKLLVVASQDGKLIVWDTYTINVKHAIPRSSLWMTCAVAPSGNFVACGGIDM 120
 QY 121 CSYSLSKSREGAVKVRELSAHTGYTSSCCRFDDNNIVVSSGDTICALMDIEQKQTVF 180
 Db 121 CSYSLSKSREGAVKVRELSAHTGYTSSCCRFDDNNIVVSSGDTICALMDIEQKQTVF 180
 QY 121 CSYLNKLRREGAVKVRVERLAGHTGILSCCRFLDDNQIVVSSGDTICALMDIEQKQTVF 180
 Db 121 CSYLNKLRREGAVKVRVERLAGHTGILSCCRFLDDNQIVVSSGDTICALMDIEQKQTVF 180
 QY 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 Db 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 QY 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 Db 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 QY 241 ICGSDASCRFLDRADQELTASHESTICGITSVATLSGRULFAGYDDNCNTWDSL 300
 Db 241 ICGSDASCRFLDRADQELTASHESTICGITSVATLSGRULFAGYDDNCNTWDSL 300
 QY 301 KCERVVLGSNDNRVSLCIGVTAADMATAVGWSWFLKWN 340
 Db 301 KCERVVLGSNDNRVSLCIGVTAADMATAVGWSWFLKWN 340
 RESULT 3 RGHUBL
 GTP-binding regulatory protein beta-1 chain - human
 N;Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-protein
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C;Accession: A24853
 R;Cocina, J.; Stengel, D.; Woo, S.L.C.; Birnbaumer, L.
 FEBS Lett. 207, 187-192, 1986
 A;Title: Beta subunits of the human liver Gs/Gi signal-transducing proteins and those of
 A;Reference number: A91368; MUID:87030912
 A;Accession: A24853
 A;Molecule type: mRNA
 A;Residues: 1-340 <COD>

A;Cross-references: GDB:X04526; NID:931667; PIDN:CAA28207.1; PID:931669
 A;Experimental source: Liver
 A;Note: The authors translated the codon GAG for residues 138 and 172 as Gln
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay signals. The beta and gamma chains, required for GTPase activity, appear to be common to all G-proteins. It is specific for each type of G protein.
 C;Genetics:
 A;Gene: GDB:GNBL1
 A;Cross-references: GDB:119279; OMIM:139380
 A;Map Position: 1p31-1p31.2
 C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology <WD3>
 C;Keywords: GTP binding; heterotrimer; signal transduction
 F;51-84/Domain: WD repeat homology <WD1>
 F;88-126/Domain: WD repeat homology <WD2>
 F;139-171/Domain: WD repeat homology <WD3>
 F;180-213/Domain: WD repeat homology <WD4>
 F;222-255/Domain: WD repeat homology <WD5>
 F;263-299/Domain: WD repeat homology <WD6>
 F;308-340/Domain: WD repeat homology <WD7>

Query Match .87.0%; Score 1573; DB 1; length 340;
 Best Local Similarity 83.2%; Pred. No. 7; e-123; Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MGEMEQOLQEAEGLKKQDADARKACADITLABLEVSLGEVGRVQMRTRRLGHAKIYA 60
 Db 1 MGEMEQOLQEAEGLKKQDADARKACADITLABLEVSLGEVGRVQMRTRRLGHAKIYA 60
 QY 61 MHWATDSKLLVVASQDGKLIVWDTYTINVKHAIPRSSLWMTCAVAPSGNFVACGGIDM 120
 Db 61 MHWATDSKLLVVASQDGKLIVWDTYTINVKHAIPRSSLWMTCAVAPSGNFVACGGIDM 120
 QY 121 CSYSLSKSREGAVKVRELSAHTGYTSSCCRFDDNNIVVSSGDTICALMDIEQKQTVF 180
 Db 121 CSYSLSKSREGAVKVRELSAHTGYTSSCCRFDDNNIVVSSGDTICALMDIEQKQTVF 180
 QY 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 Db 181 VGHGDGMSLAVSPDKYLFETSGACASAKLWDVGRGTCQTFQFGHESINAICFFPNEA 240
 QY 241 ICGSDASCRFLDRADQELTASHESTICGITSVATLSGRULFAGYDDNCNTWDSL 300
 Db 241 ICGSDASCRFLDRADQELTASHESTICGITSVATLSGRULFAGYDDNCNTWDSL 300
 QY 301 KCERVVLGSNDNRVSLCIGVTAADMATAVGWSWFLKWN 340
 Db 301 KCERVVLGSNDNRVSLCIGVTAADMATAVGWSWFLKWN 340
 RESULT 4 RGBOBL
 GTP-binding regulatory protein beta-1 chain - bovine
 N;Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-protein
 C;Species: Bos primigenius tauris (cattle)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C;Accession: A24547
 R;Sugimoto, K.; Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Minamino, N.; Kangaw FBS Lett. 191, 235-240, 1985
 A;Title: Primary structure of the beta-subunit of bovine transducin deduced from the
 A;Reference number: A24225; MUID:86030675
 A;Accession: A24225
 A;Molecule type: mRNA
 A;Residues: 1-340 <SUG>
 A;Cross-references: GDB:X03073
 R;Bong, H.K.W.; Hurley, J.B.; Hopkins, R.S.; Miale-Lye, R.; Johnson, M.S.; Doolittle, Proc. Natl. Acad. Sci. U.S.A. 83, 2162-2166, 1986
 A;Title: Repetitive segmental structure of the transducin beta subunit: homology with
 A;Reference number: A25457; MUID:86177563
 A;Accession: A25457
 A;Molecule type: mRNA
 A;Residues: 1-340 <POX>

Fri Sep 28 10:45:08 2001

A: Cross-references: GB: M13236; NID: g163782; PIDN: AAA30792_1; PID: g163783
C: Comment: The G proteins are a family of guanine nucleotide-binding proteins that relax airways. It is specific for each type of G protein.

C: Comment: In mammals, four distinct types of beta chains have been found.

C: Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology <WD1>
C: Keywords: GTP binding; heterotrimer; signal transduction

F; 51-84 /Domain: WD repeat homology <WD2>

F; 88-171 /Domain: WD repeat homology <WD3>

F; 139-171 /Domain: WD repeat homology <WD4>

F; 180-213 /Domain: WD repeat homology <WD5>

F; 222-255 /Domain: WD repeat homology <WD6>

F; 263-299 /Domain: WD repeat homology <WD7>

F; 308-340 /Domain: WD repeat homology <WD7>

Query Match 87.0%; Score 1573; DB 1; Length 340;

Best Local Similarity 83.2%; Pred. No. 7.9e-123; Mismatches 26; Indels 0; Gaps 0;
 Matches 283; Conservative 31; MisMatches 26; Indels 0; Gaps 0;

QY 1 MGEMEQLKQEAEQDQKQIADARKACADITLAELVSLGLEYGRVQMRTRTGLRHLAKIYA 60
 Db 1 MSELDQRLQEAEQKQIADARKACADATLSQINNNDPVGRIQRTRTRLGHAKIYA 60

QY 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLASSWMTCAVAPSGNFVACGGDNM 120

Db 61 MHWGTDSRLVLVSASQDGKLLIWDSYTNNKHAIPPLASSWMTCAVAPSGNFVACGGDNM 120

QY 121 CSYIYSKSRQGVNVSKRELSAHDGYLSCLRFDDNNVTSSGDTCALWDIETGQKTF 180

Db 121 CSYIYNLKTRQGVNVSKRELSAHDGYLSCLRFDDNNVTSSGDTCALWDIETGQKTF 180

QY 181 VGHGDMSLAVSPYKLFISGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240

Db 181 VGHGDMSLAVSPYKLFISGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240

QY 181 TGTGDDMSLALPDRFLFVSGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240

Db 181 TGTGDDMSLALPDRFLFVSGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240

QY 241 ICGSDDASCRFLDRADQELTAYSHESTIGITSVAFSLSGRLFAGYDDPNCNWDSL 300

Db 241 FATSDDATCRFLDRADQELMTYSHDNITCGITSVSFSKGRLILLAGYDDFNCDYDAL 300

QY 301 KCEVGVLTSGHDRVSLCGLVTAQGMAVATGSWDFSLKIWN 340

RESULT 5
 JC5057
 G protein beta 1 - mouse
 C; Species: Mus musculus (house mouse)
 C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Aug-1999
 C; Accession: JC5057
 R; Oiu: R.; Schimmer, B.P.

Gene 175, 275-277, 1996
 A; Title: CDNA for the beta 1 subunit of quanylnucleotide-binding regulatory proteins from mouse
 A; Reference number: JC5057; MUID: 97074684
 A; Accession: JC5057
 A; Status: nucleic acid sequence not shown
 A; Residues: 1-340 <Q1U>
 A; Cross-references: GB: U29055; NID: g9868168; PIDN: AAC52905.1; PID: 9868169
 A; Molecule type: mRNA
 A; Gene: GNB2
 A; Residues: 1-340 <GAO>
 A; Cross-references: GB: M16538
 C; Comment: The G proteins are a family of guanine nucleotide-binding proteins that regulate airways. It is specific for each type of G protein.

A; Residues: 1-340 <Q1U>

A; Cross-references: GB: M16538

C; Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology

C; Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology <WD1>

C; Keywords: GTP binding; heterotrimer; signal transduction

F; 1-84 /Domain: WD repeat homology <WD2>

F; 88-126 /Domain: WD repeat homology <WD3>

F; 139-171 /Domain: WD repeat homology <WD4>

F; 180-213 /Domain: WD repeat homology <WD5>

F; 222-255 /Domain: WD repeat homology <WD6>

F; 263-299 /Domain: WD repeat homology <WD7>

F; 308-340 /Domain: WD repeat homology <WD7>

Matches 283; Conservative 31; MisMatches 26; Indels 0; Gaps 0;
 QY 1 MGEMEQLKQEAEQDQKQIADARKACADITLAELVSLGLEYGRVQMRTRTGLRHLAKIYA 60
 Db 1 MSELDQRLQEAEQKQIADARKACADATLSQINNNDPVGRIQRTRTRLGHAKIYA 60

QY 61 MHWATDSKLVLVSASQDGKLIWDTYTNNKHAIPPLASSWMTCAVAPSGNFVACGGDNM 120
 Db 61 MHWGTDSRLVLVSASQDGKLLIWDSYTNNKHAIPPLASSWMTCAVAPSGNFVACGGDNM 120

QY 121 CSYIYSKSRQGVNVSKRELSAHDGYLSCLRFDDNNVTSSGDTCALWDIETGQKTF 180
 Db 121 CSYIYNLKTRQGVNVSKRELSAHDGYLSCLRFDDNNVTSSGDTCALWDIETGQKTF 180

QY 181 VGHGDMSLAVSPYKLFISGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240
 Db 181 VGHGDMSLAVSPYKLFISGADASAKLWDYFREGTCRQTGHSIDNAICFPNGEA 240

QY 241 ICGSDDASCRFLDRADQELTAYSHESTIGITSVAFSLSGRLFAGYDDPNCNWDSL 300
 Db 241 FATSDDATCRFLDRADQELMTYSHDNITCGITSVSFSKGRLILLAGYDDFNCDYDAL 300

QY 301 KCEVGVLTSGHDRVSLCGLVTAQGMAVATGSWDFSLKIWN 340

RESULT 6
 RGHUB2
 GTP-binding regulatory protein beta-2 chain - human
 C; Species: Homo sapiens (man)
 C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C; Accession: B26617; B28040
 R; Fong, H.K.W.; Amatruada, T.T.; Birren, B.W.; Simon, M.I.
 Proc. Natl. Acad. Sci. U.S.A., 84, 3792-3796, 1987
 A; Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins identified
 A; Reference number: A94155; MUID: 87231903
 A; Accession: B26617
 A; Molecule type: mRNA
 A; Residues: 1-340 <FOO>
 A; Cross-references: GB: M16514; NID: g183469; PIDN: AAC03179.1; PID: 9386751
 R; Gro, B.; Gilman, A.G.; Robishaw, J.D.
 Proc. Natl. Acad. Sci. U.S.A., 84, 6122-6125, 1987
 A; Title: A second form of the beta subunit of signal-transducing G proteins.
 A; Reference number: A94177; MUID: 87317607
 A; Accession: B28040
 A; Molecule type: mRNA
 A; Residues: 1-340 <GAO>
 A; Cross-references: GB: M16538
 C; Comment: The G proteins are a family of guanine nucleotide-binding proteins that regulate airways. It is specific for each type of G protein.

C; Comment: In mammals, four distinct types of beta chains have been found.

C; Genetics:

A; Gene: GDB:GNB2

A; Cross-references: GDB:120004; OMIM: 139390

A; Cross-references: GDB:120004; OMIM: 139390

A; Map position: 7q21.3-q22.1

C; Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C; Keywords: GTP binding; heterotrimer; signal transduction

F; 1-84 /Domain: WD repeat homology <WD2>

F; 88-126 /Domain: WD repeat homology <WD3>

F; 139-171 /Domain: WD repeat homology <WD4>

F; 180-213 /Domain: WD repeat homology <WD5>

F; 222-255 /Domain: WD repeat homology <WD6>

F; 263-299 /Domain: WD repeat homology <WD7>

F; 308-340 /Domain: WD repeat homology <WD7>

Query Match 84.2%; Score 1523; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 1.e-118; Mismatches 34; Indels 0; Gaps 0;
 Matches 275; Conservative 31; MisMatches 34; Indels 0; Gaps 0;

QY 1 MGEMEQLQEAEQQLKKQTADARKACADITLAELVSGLEVYGRVOMTRTRLGHAKIYA 60
Db 1 MSELQDQLRQAEBOLQKSRQEARSKAANDTTLATVASSNLEPIGTRIOMTRRTLGHAKIYA 60
QY 61 MHWATDSKLVLVSAQDGKLIVWDTYTINKVHAIPRSSLWMTCAVAPSGNFVAGGLDM 120
Db 61 MHWASDRNLVSAQDGKLIVWDTYTINKVHAIPRSSLWMTCAVAPSGNFVAGGLDM 120
QY 121 CSYSLKTRREGNRVSYRELSAHTGLSCCRFLDDNNITSSGDTALWDIETGQOKTVE 180
Db 121 CSYSLKTRREGNRVSYRELSAHTGLSCCRFLDDNNITSSGDTALWDIETGQOKTVE 180
QY 181 VGHGDGMSLAVSPYKLFISGACDASKLWDIETGQOKTVE 180
Db 181 VGHGDGMSLAVSPYKLFISGACDASKLWDIETGQOKTVE 180
QY 241 ICGSDDAASCRLFDLRADELTAYSHESICGTSVAFSLSGRLLFAGYDFFNCNWDSL 300
Db 241 ICGSDDAASCRLFDLRADELTAYSHESICGTSVAFSLSGRLLFAGYDFFNCNWDSL 300
QY 301 KCERGVLSLHDNRVSYCLGVTADGMATGSMDSFLKIWN 340
Db 301 KGDRAVLAGHNDKRVSCLGVTIDGMATGSMDSFLKIWN 340

RESULT 7
T20830 hypothetical protein F13D12.7 - Caenorhabditis elegans
C;Species: C.elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: T20830
R;Coles, L.
A;Reference number: 219330
A;Accession: T20830
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <WIL>
A;Cross-references: EMBL:X1797; PID:NID:9642; PID:CAA35532; 1; PID:96643
A;Experimental source: clone F13d12
C;Genetics:
A;Gebe: CESP:F13D12.7
A;Map position: 2
A;Introns: 19/3; 57/3; 89/3; 116/1; 166/2; 209/3; 233/3; 305/1
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
Query Match 84.0%; Score 1520; DB 2; Length 340;
Best Local Similarity 81.2%; Pred. No. 1.9e-18; Length 340;
Matches 276; Conservative 31; Mismatches 33; Indels 0; Gaps 0;
QY 1 MGEMEQLQEAEQQLKKQTADARKACADITLAELVSGLEVYGRVOMTRTRLGHAKIYA 60
Db 1 MSELQDQLRQAEBOLQKSRQEARSKAANDTTLATVASSNLEPIGTRIOMTRRTLGHAKIYA 60
QY 61 MHWATDSKLVLVSAQDGKLIVWDTYTINKVHAIPRSSLWMTCAVAPSGNFVAGGLDM 120
Db 61 MHWASDRNLVSAQDGKLIVWDTYTINKVHAIPRSSLWMTCAVAPSGNFVAGGLDM 120
QY 121 CSYSLKTRREGNRVSYRELSAHTGLSCCRFLDDNNITSSGDTALWDIETGQOKTVE 180
Db 121 CSYSLKTRREGNRVSYRELSAHTGLSCCRFLDDNNITSSGDTALWDIETGQOKTVE 180
QY 181 VGHGDGMSLAVSPYKLFISGACDASKLWDIETGQOKTVE 180
Db 181 VGHGDGMSLAVSPYKLFISGACDASKLWDIETGQOKTVE 180
QY 301 KCERGVLSLHDNRVSYCLGVTADGMATGSMDSFLKIWN 340
Db 301 KGDRAVLAGHNDKRVSCLGVTIDGMATGSMDSFLKIWN 340

RESULT 8
Db 301 RQERAGVLAGHNDNRVSYCLGVTEDGMAVCTGSWDSFLKIWN 340

RESULT 9
RGSB4
GTP-binding regulatory protein beta-4 chain - mouse
N;Alternate names: guanine nucleotide binding protein beta-4 chain; heterotrimeric G-protein
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: J50669
R;von Weizsaecker, E.; Strathmann, M.P.; Simon, M.I.
Biochem. Biophys. Res. Commun. 183, 350-356, 1992

A;Title:	Diversity among the beta subunits of heterotrimeric GTP-binding proteins: characterization
A;Reference number:	JS0669; MOID:92181467
A;Molecule type:	mRNA
A;Residues:	1-340 <NON>
B;Cross-references:	GB:SB6124; NID:924669; PIDN:AA21609_1; PID:g246470
C;Comment:	The G proteins are a family of guanine nucleotide-binding proteins that relay signals. The beta and gamma chains, required for GTPase activity, appear to be common to all. It is specific for each type of G protein.
C;Comment:	In mammals, four distinct types of beta chains have been found.
C;Superfamily:	GTP-binding regulatory protein beta chain; WD repeat homology <WD1>
C;Keywords:	GTP binding; heterotrimer; signal transduction
F;51-84/Domain:	WD repeat homology <WD5>
F;88-126/Domain:	WD repeat homology <WD6>
F;139-171/Domain:	WD repeat homology <WD3>
F;180-213/Domain:	WD repeat homology <WD4>
F;222-255/Domain:	WD repeat homology <WD5>
F;263-399/Domain:	WD repeat homology <WD6>
F;308-340/Domain:	WD repeat homology <WD7>
Query Match	82.5%; Score 1493; DB 1; Length 340;
Best Local Similarity	79.1%; Pred. No. 3_3e-16;
Matches	269; Conservative 37; Mismatches 34; Indels 0; gaps 0;
Qy	1 MGEMEOLKQEASQKKQIAADARKACADITLAELVSLGLEVGRVQMRTRRLGHAKYA 60
Db	1 MSELEQLKQEAEQDLRNOIQDARKACKNDATLQVITSNADSVGRIQMRTRRLGHAKYA 60
Qy	61 MHMADTSKLVLVASQDGKLUVMDTYTENKWHAPLRLSSWMMTCAYABPSGNFVACGGDNM 120
Db	61 MHMGYDSRLLVSAQSODGKLUWDSYTINMMHAIPRLRSSWMMTCAYAAGSGNNVACGGDNM 120
Qy	121 CSYLSLKSEGNYKVSRSAHUGYLSGCCRELDDNTVTSGGITTCALWDIENGQKTVF 180
Db	121 CSYLNLTKEGDKVRSRELAGHTYCLSCRGFLDQGQTTSGGITTCALWDIENGQKTVF 180
Qy	181 VGHGDCMASLAVSDYKLTISGACDASAKLWDYREGICRQTFGHESDNATCFFPGEA 240
Db	181 TGHSDGYMSLSDPLKTVSAGCDAKSLLKWDIRDGMCHQSFTHGHSIDINAFFPSGA 240
Qy	241 ICTGSDASDASCRLFDLRAQDDELTAHSHESTICGTISVAFASSGRLLFGAGYDDFNQNVWDSL 300
Db	241 PATGSDDAICRGLFDLRAQDPELLYSHDNQITGITSVAASSKSGRLLLAGYDDFNCSWMDAL 300
Qy	301 KCERYGVLSCHDRVSYCLG3TADGMAVATGSWDSLFLKINN 340
Db	301 KGGRSQVLAGHDNRVSYCLGVTDDGMAVATGSWDSLFLRINN 340
RESULT	10
S34348	GRP-binding regulatory protein beta chain - great pond snail
N;Alternate names:	guanine nucleotide regulatory protein beta chain
C;Species:	Lymnaea stagnalis (great pond snail)
C;Date:	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession:	S69891; S33438
R;Knol, J.C.; Roovers, E.; van Kesteren, E.R.; Planta, R.J.; vreugdenhil, E.; van Heerikhuizen, B.; Biophys. Acta 1222, 129-133, 1994	Title: A G-protein beta subunit that is expressed in the central nervous system of the
A;Title:	A G-protein beta subunit that is expressed in the central nervous system of the
A;Reference number:	JS69891; MUID:94242793
A;Accession:	S69891
A;Status:	preliminary
A;Molecule type:	mRNA
A;Residues:	1-341 <KN2>
A;Cross-references:	EMBL:223105; NID:931631; PIDN:CAA86652_1; PID:9312632
C;Superfamily:	GRP-binding regulatory protein beta chain; WD repeat homology
F;52-85/Domain:	WD repeat homology <WD1>
F;181-214/Domain:	WD repeat homology <WD4>
F;267-300/Domain:	WD repeat homology <WD5>
F;309-341/Domain:	WD repeat homology #status atypical <WD7>

Fri Sep 28 10:45:08 2001

us-09-492-029-3.rpr

Fri Sep 28 10:45:11 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:21 ; Search time 34.79 Seconds
 Scoring table: BLOSUM62 (without alignments)
 Searched: GapP 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 412676
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

```

A-Geneseq_0601:*
1: /SIDS8/gcadata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcadata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcadata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcadata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcadata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcadata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcadata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcadata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcadata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcadata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcadata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcadata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcadata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcadata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcadata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcadata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcadata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcadata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcadata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcadata/geneseq/geneseqp/AA2000.DAT:*
21: /SIDS8/gcadata/geneseq/geneseqp/AA2001.DAT:*
22: /SIDS8/gcadata/geneseq/geneseqp/AA2001.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1809	100.0	340	Human G protein beta Human Taste Cell S
2	1809	100.0	21	Human Hgb3 G-prot Human Hgb3 G-pro
3	1809	100.0	340	Mutant human Taste Mutant human Taste
4	1807	99.9	340	Mutant human Taste Mutant human Taste
5	1805	99.8	340	Mutant human Taste Mutant human Taste
6	1806	99.8	340	Mutant rat Taste C Mutant rat Taste C
7	1765	97.6	340	Rat Taste Cell spe Rat Taste Cell spe
8	1762	97.4	340	Mutant rat Taste C Mutant rat Taste C
9	1759	97.2	340	Mutant rat Taste C Mutant rat Taste C
10	1758	97.2	340	WD-40 domain-contg C WD-40 domain-contg C
11	1758	87.2	340	ARR85059 ARR85059

SUMMARIES

12	1578	87.2	340	21	RAY67863	nuclen	Human
13	1558.5	86.2	209	19	AMW5364	G-protein be	
14	1548.5	85.5	297	21	AWW09359	Human G-protein be	
15	1528	84.5	340	16	AAR85863	WD-40 domain-contg	
15	1528	84.5	340	21	AYX67864	Human Rgb2 G-prot	
15	1528	84.5	340	21	AYX67864	Mouse Mgb2 G-prot	
15	1500	82.9	340	21	AYX67866	WD-40 domain-contg	
17	1463	80.9	341	16	AAR85866	WD-40 domain-contg	
18	1459	80.7	340	16	AAR85861	WD-40 domain-contg	
19	1459	78.6	326	16	AAR85860	Human cell cycle r	
20	1421	52.5	395	20	AYX31732	Mouse Mgb5 G-prot	
21	949.5	52.4	353	21	AYX67867	Human pancreatic c	
22	948.5	52.4	371	21	AAB54247	Gene 45 human secr	
23	905.5	50.1	295	22	AAB5330	Human secreted pro	
24	865.5	48.0	295	22	AAB75331	Arabidopsis thalia	
25	863.5	47.8	295	21	AAB39215	Gene 45 human secr	
26	815.5	45.1	377	21	AAB75332	Yeast G protein be	
27	658.5	36.4	229	22	AAB75332	WD-40 domain-contg	
28	650	35.9	422	16	AAR85876	Ste6/Gbeta intera	
29	650	35.9	423	21	AYX67890	Yeast G protein be	
30	650	35.9	423	20	AAW98103	Yeast Ste6 protein	
31	649	35.9	422	21	AYY67862	Yeast G protein be	
32	647.5	35.8	423	20	AAW98104	Arabidopsis thalia	
33	646	35.7	422	21	AAG16503	Arabidopsis thalia	
34	645.5	35.7	267	21	AAG39216	Arabidopsis thalia	
35	645.5	35.7	267	21	AAG39216	Human secreted pro	
36	612.5	33.9	225	22	AAB75333	Breast and ovarian	
37	597	32.9	243	21	AAB58974	Human cancer assoc	
38	568	31.4	166	21	AAB43691	Arabidopsis thalia	
39	524	29.0	227	21	AAG16504	Arabidopsis thalia	
40	524	29.0	227	21	AYG39217	Arabidopsis thalia	
41	422.5	23.4	203	21	AAC35537	Arabidopsis thalia	
42	308	17.0	333	21	AAG05554	Receptor of activa	
43	305.5	16.9	317	16	AAB85850	WD-40 domain-contg	
44	16.9	317	16	16	AAR85862	WD-40 domain-contg	
16	317	16	16	16	AAR85867		

XX	CC	This sequence represents the human G-protein beta 3 subunit. A variant of the gene encoding this protein has applications in the diagnosis of diseases or assessing the risk of a disease associated with G-protein misregulation. G-protein misregulation is associated with hypertension, cardiovascular diseases e.g. coronary heart disease, atherosclerosis, restenosis, stroke and thrombosis, metabolic disorders such as diabetes, diabetic complications, disorders of lipid metabolism and central chemoreception dysfunction (e.g. sudden infant death syndrome), and immunological disorders such as impaired wound healing, tumours, AIDS, cirrhosis and transplant rejection.
SQ	Sequence 340 AA;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MGEMEQLROEAEQIKKOTADAKRACADVTALVELSGLEWGRVQMRTRTLRGHLAKIYA 60	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 mgemeqleqrgeaqdkkqkqadarkacadvtaelvsglevgrvqmrtrtlrghlakiya 60	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	61 MHWAIDSKLIVSASQDGKLIWDSYNTNKHAIPRLRSSVMTCAYAAPSAGNTVA,CGSLDNM 120	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	61 mhwaidsklivsasqdgkliwdsyntnkhaiprlrssvmtcayapsagnfvcaggldnm 120	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	121 CSYLNLSREGNVKVSRELAAHTGVLSCRELDNNVTSSGDTTCAWLWIEETSGKTVF 180	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	121 csynlnksregnvksrelaahtgvlscrcldnnvtssgdttcawlwietsgktvf 180	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	181 VGTGDDMSLAVSPDNLFSGACDASAKLWDREGCQRTFGHSDINACFPNGA 240	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	181 vgtgdmslavspdnlfsgacdasklwdregcqrftghsdinaicfpng 240	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	241 IGTGSDASCLFDLRADOBELICFSHESITCTSYAFSISGRLLFAGDDFNQNVNDSM 300	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	241 ictgsdadasclfdlradobelicshesitctsyafsisgrllfagddfnqnvndsm 300	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	301 KSERVGLLSGDHNRVSCIGVATDGMAVATGSWDSFLKIWN 340	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	301 kservgilsgdhnrvscligvtagmavatgswdslkiwn 340	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	2	RESULT 2
ID	AAB15169	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	AAB15169 standard; Protein; 340 AA.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	AAB15169;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	12-DEC-2000 (first entry)	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE	Human Taste Cell specific G-protein beta 3 subunit.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW	Human: Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW	taste transduction pathway; pharmaceutical; food industry.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Homo sapiens.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PN	W020045179-A2.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PD	03-AUG-2000.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	26-JAN-2000; 2000WO-US02218.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	27-JAN-1999; 99US-0117404.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(RGGC) UNTV CALIFORNIA.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PI	Zuker CS, Adler JE, Lindemeier J;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	WTI; 2000-499361-/44.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	N-PSDB; AAN74591.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(LEBU/) DEBERER E.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(LEBU/) LEEDW T.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	CC	Identifying a compound that modulates sensory signaling in sensory cells for use in pharmaceutical and food industries comprises contacting the compound with a sensory cell specific G-protein beta polypeptide -
PT	PT	polypeptide -
PT	PT	claim 1; Page 63; 68pp; English.
XX	CC	The present sequence is human G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for pharmaceutical and food industries to customise taste.
SQ	Sequence 340 AA;	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MGEMEQLROEAEQIKKOTADAKRACADVTALVELSGLEWGRVQMRTRTLRGHLAKIYA 60	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 mgemeqleqrgeaqdkkqkqadarkacadvtaelvsglevgrvqmrtrtlrghlakiya 60	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	61 MHWAIDSKLIVSASQDGKLIWDSYNTNKHAIPRLRSSVMTCAYAAPSAGNTVA,CGSLDNM 120	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	61 mhwaidsklivsasqdgkliwdsyntnkhaiprlrssvmtcayapsagnfvcaggldnm 120	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	121 CSYLNLSREGNVKVSRELAAHTGVLSCRELDNNVTSSGDTTCAWLWIEETSGKTVF 180	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	121 csynlnksregnvksrelaahtgvlscrcldnnvtssgdttcawlwietsgktvf 180	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	181 VGTGDDMSLAVSPDNLFSGACDASAKLWDREGCQRTFGHSDINACFPNGA 240	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	181 vgtgdmslavspdnlfsgacdasklwdregcqrftghsdinaicfpng 240	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	241 IGTGSDASCLFDLRADOBELICFSHESITCTSYAFSISGRLLFAGDDFNQNVNDSM 300	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	241 ictgsdadasclfdlradobelicshesitctsyafsisgrllfagddfnqnvndsm 300	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	301 KSERVGLLSGDHNRVSCIGVATDGMAVATGSWDSFLKIWN 340	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	301 kservgilsgdhnrvscligvtagmavatgswdslkiwn 340	Query Match Best Local Similarity 100.0%; Score 1809; DB 21; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	3	RESULT 3
ID	AX67865	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	AAV67865	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	25-APR-2000 (first entry)	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE	Human Hbb3 G-protein beta3 subunit amino acid sequence.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW	St20P/PAK: G-protein-coupled receptor signal transduction; human; Hbb3;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KW	St20P/Cbeta interaction domain; p21-activated protein kinase;	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Homo sapiens.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PN	CR221995-8-Al.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PD	07-JUL-1999.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	07-JAN-1998; 98CA-2219958.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(LEBU/) DEBERER E.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(LEBU/) LEEDW T.	Query Match Best Local Similarity 100.0%; Score 1809; DB 19; Length 340; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PA	(THOM/)	THOMAS D Y.	FT	Misc-difference 7 /note= "Wild-type Ieu substituted by Ile"
PA	(WHIT/)	WHITEWAY M.	FT	
XX			XX	
PI	Lebreer E,	Leeuw T,	PN	WO20045179-A2.
XX			XX	
DR	WPI:	2000-137553/13.	PN	03-AUG-2000.
XX			XX	
PT	Interacting polypeptides involved in G-protein-coupled receptor signal		PF	26-JAN-2000; 2000WO-US02218.
PT	transduction		XX	
PT			PR	27-JAN-1999; 99US-0117404.
XX			XX	
PS	Claim 3; Fig 6; 91pp; English.		PA	(REGC) UNIV CALIFORNIA.
XX			XX	
CC	This sequence represents the beta3 subunit of a human G-protein. The invention relates to the G-protein beta subunit interaction domain of the Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein kinases are p21-activated protein kinases (PAK), and they are involved in many varied cellular processes ranging from morphogenesis and stress response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and Ste20p/PAK are useful for designing in vitro and in vivo experimental models which enable the screening of large collections of synthetic, semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta and Ste20p/PAK dependent diseases.		PI	Zuker CS, Adler JE, Lindemeier J;
CC			XX	
Matches 340; Conservative	Score 1809; DB 21; Length 340; Best Local Similarity 100.0%; Pred. No. 5.3e-171; Indels 0; Gaps 0; Mismatches 0;		DR	WPI; 2000-499361/44.
QY	1 MGEMEQIQLRQEAEQLKKQIADARKACADVTLAELVSGLEVGVRQMRTRTLRGHLAKIYA 60		XX	
Db	1 mgemeqirqeaeqlkkqiadarkacadvtlaelvsglevrgvqrmttrtlrghlakiya 60		PT	Identifying a compound that modulates sensory signaling in sensory cells for use in pharmaceutical and food industries comprises contacting the compound with a sensory cell specific G-protein beta polypeptide -
QY	61 MHWATDSKLVLVASQDGKLIWDSYTNTNKHAIPIRSSWMTCAYAPSNEVAGGIDNM 120		XX	
Db	61 mhawatdsklvlvasqdgkliwdsyttnkhaiplrsswmvcayapsnfvcaggidnm 120		PS	Disclosure; Page - ; 68pp; English.
QY	121 CSRNLNKSREGNWKVRSRELSAHTGYLSCCREFLDDNNNIVSSGDTTCAALMDIERGOQKVF 180		XX	
Db	121 csinlnksregnkvrsrealsantgylscrcrfddnnivssgdttcalwdietggktvf 180		CC	The present sequence is a mutant human G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customize taste.
QY	181 VGHGDCMSLAVASPDENFLPISGACDASAKLWDYREGCROTTGHESDINACIFFPNEA 240		CC	Note: The present sequence is not shown in the specification given on page 63 derived from the human wild-type TC-Gbeta3 sequence (see AAB15169) and information given on page 8 of the disclosure.
Db	181 vghtgdcmaslavspdnflpisgacdasaklwdrregctqftgnesdinaciffpne 240		CC	
QY	241 ICTGSDASCRLLRADDELTSFHSHESTICGITSVAFSLSGRFLPAGYDFNCNWDSM 300		XX	
Db	241 ictgsdasscrldradgelicfhesicgitsvafslgrlfagyddnenvwdsm 300		PS	Sequence 340 AA;
QY	301 KSERVGLSLGDHNDRVSCLGTVADGMAVATGSWSFLKIN 340		XX	
Db	301 kseervgilsgdnhrvsclgtvadgmatgwsflkiwn 340		CC	The present sequence is a mutant human G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customize taste.
RESULT 4			DB	Score 1807; DB 21; Length 340; Best Local Similarity 99.9%; Pred. No. 8.4e-171; Indels 0; Gaps 0; Mismatches 1;
ID	ABI15173 standard; Protein; 340 AA.		DB	1 mgemeqirqeaeqlkkqiadarkacadvtlaelvsglevrgvqrmttrtlrghlakiya 60
XX			QY	61 MHWATDSKLVLVASQDGKLIWDSYTNTNKHAIPIRSSWMTCAYAPSNEVAGGIDNM 120
AC	ABI15173;		Db	61 mhawatdsklvlvasqdgkliwdsyttnkhaiplrsswmvcayapsnfvcaggidnm 120
XX			QY	121 CSRNLNKSREGNWKVRSRELSAHTGYLSCCREFLDDNNNIVSSGDTTCAALMDIERGOQKVF 180
DE	12-DEC-2000 (first entry)		Db	121 csinlnksregnkvrsrealsantgylscrcrfddnnivssgdttcalwdietggktvf 180
XX			QY	181 VGHGDCMSLAVASPDENFLPISGACDASAKLWDYREGCROTTGHESDINACIFFPNEA 240
XX			Db	181 vghtgdcmaslavspdnflpisgacdasaklwdrregctqftgnesdinaciffpne 240
XX			QY	241 ICTGSDASCRLLRADDELTSFHSHESTICGITSVAFSLSGRFLPAGYDFNCNWDSM 300
XX			Db	241 ictgsdasscrldradgelicfhesicgitsvafslgrlfagyddnenvwdsm 300
XX			QY	301 KSERVGLSLGDHNDRVSCLGTVADGMAVATGSWSFLKIN 340
XX			Db	301 kseervgilsgdnhrvsclgtvadgmatgwsflkiwn 340
XX			RESULT 5	
KW	Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3; taste transduction pathway; pharmaceutical; food industry; mutation; mutent; mutant.		ID	ABI15174
XX			XX	AAB15174 standard; Protein; 340 AA.
OS	Homo sapiens.		DB	241 ICTGSDASCRLLRADDELTSFHSHESTICGITSVAFSLSGRFLPAGYDFNCNWDSM 300
OS	Synthetic.		QY	301 KSERVGLSLGDHNDRVSCLGTVADGMAVATGSWSFLKIN 340
XX			Db	301 kseervgilsgdnhrvsclgtvadgmatgwsflkiwn 340
FH	Key	Location/Qualifiers	DT	12-DEC-2000 (first entry)

DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #2.
 XX
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 XX
 OS Homo sapiens.
 XX Synthetic.

PH Key
 FT Misc-difference 161 Location/Qualifiers
 XX /note= "Wild-type Ser substituted by Thr"
 PN WO200045179-A2.
 XX
 PD 03-AUG-2000.
 XX
 PT 26-JAN-2000; 2000WO-US02218.
 XX PR 27-JAN-1999; 99US-0117404.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Zuker CS, Adler JE, Lindemer J;
 DR XX WPI; 2000-499361/44.
 XX
 PT Identifying a compound that modulates sensory signaling in sensory
 cells for use in pharmaceutical and food industries comprises
 contacting the compound with a sensory cell specific G-protein beta
 polypeptide -
 PT Disclosure; Page - ; 68PP; English.
 XX
 CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC Sequence 1S referred to as taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC Note: The present sequence is not shown in the specification but is
 derived from the human wild-type TC-Gbeta3 sequence given on page 63
 (see AB15169) and information given on page 8 of the disclosure.
 XX Sequence 340 AA;

Query Match Best Local Similarity 99.8%; Score 1805; DB 21; Length 340;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAREQKKQIADARKACADVTLAELVSGLEVGVRVQMRTRRLGHAKIYA 60
 Db 1 mgemeqirqeaeqkkqiadarkacadvtlaelvsglevgrvqmrtrrlghakiya 60
 QY 61 MHWATSKLLVSASDQKLITWDSYTNNKHAIPRLRSSWVMTCAVAPSGNEVACGGIDNM 120
 Db 61 mhawatdkllvsasdgklltwdsyttnkvhaiprlsswvmtcavapsgnfvacggldnm 120
 QY 121 CSINYIKSREGNVKVSRELSAHTGVLSCCREFDNNNTVSSGTTCALWDIETGQKTVF 180
 Db 121 csiyiniksregnvkvsrelsahtgvlscrcrfddnnntvssgttcalwdietgqktvf 180
 QY 181 VQHTGOCMSLAVIDSPDPFLNFTISGACDASKLWDYREGRCRQRTGHSDDINACICFPNGEA 240
 Db 181 vqhtgocmslavspdpflnifsgacdasklwdvregrcrqtgtghesdinacicfpngea 240
 QY 241 ICGSDASCRDFRADOLELICFSHESIIGCTWSAFSLSCRLLPAGYDDFNCRNWDSM 300
 Db 241 ictgsdascrdfraoleliscfshesiicgtsafslscrllpagsyddfncrenwdsm 300
 QY 301 KSERVGLSGHDNRVSCLGVTADGMAVATGSMDSFVKIWN 340
 XX

Db 301 kservglsghdnrvcslgvtdgmvatgsmdsfvkwn 340

RESULT 6

ID AAB15175
 ID AAB15175 standard; protein; 340 AA.
 AC AAB15175;
 AC
 DT 12-DEC-2000 (first entry)

DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.
 XX
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 XX
 OS Homo sapiens.
 XX Synthetic.

PH Key
 FT Misc-difference 301 Location/Qualifiers
 XX /note= "Wild-type Lys substituted by Arg"
 PN WO200045179-A2.
 XX
 PD 03-AUG-2000.
 XX PR 26-JAN-2000; 2000WO-US02218.
 XX PR 27-JAN-1999; 99US-0117404.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Zuker CS, Adler JE, Lindemer J;
 DR XX WPI; 2000-499361/44.
 XX
 PT Identifying a compound that modulates sensory signaling in sensory
 cells for use in pharmaceutical and food industries comprises
 contacting the compound with a sensory cell specific G-protein beta
 polypeptide -
 PT Disclosure; Page - ; 68PP; English.
 XX
 CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC Sequence 1S referred to as taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC Note: The present sequence is not shown in the specification but is
 derived from the human wild-type TC-Gbeta3 sequence given on page 63
 (see AB15169) and information given on page 8 of the disclosure.
 XX Sequence 340 AA;

Query Match Best Local Similarity 99.8%; Score 1805; DB 21; Length 340;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAREQKKQIADARKACADVTLAELVSGLEVGVRVQMRTRRLGHAKIYA 60
 Db 1 mgemeqirqeaeqkkqiadarkacadvtlaelvsglevgrvqmrtrrlghakiya 60
 QY 61 MHWATSKLLVSASDQKLITWDSYTNNKHAIPRLRSSWVMTCAVAPSGNEVACGGIDNM 120
 Db 61 mhawatdkllvsasdgklltwdsyttnkvhaiprlsswvmtcavapsgnfvacggldnm 120
 QY 121 CSINYIKSREGNVKVSRELSAHTGVLSCCREFDNNNTVSSGTTCALWDIETGQKTVF 180
 Db 121 csiyiniksregnvkvsrelsahtgvlscrcrfddnnntvssgttcalwdietgqktvf 180
 QY 181 VQHTGOCMSLAVIDSPDPFLNFTISGACDASKLWDYREGRCRQRTGHSDDINACICFPNGEA 240
 Db 181 vqhtgocmslavspdpflnifsgacdasklwdvregrcrqtgtghesdinacicfpngea 240
 QY 241 ICGSDASCRDFRADOLELICFSHESIIGCTWSAFSLSCRLLPAGYDDFNCRNWDSM 300
 Db 241 ictgsdascrdfraoleliscfshesiicgtsafslscrllpagsyddfncrenwdsm 300
 QY 301 KSERVGLSGHDNRVSCLGVTADGMAVATGSMDSFVKIWN 340
 XX

Db 301 kservglsghdnrvcslgvtdgmvatgsmdsfvkwn 340

Db 121 csiylkksregnkvksrelsahytyscrfiddannivtssgattcalwdietggktvf 180
 QY 181 VGHGDCMSLAVSPDNFLFSGACDASAKLWVREGTCRQFTGHESDINATCFFPNEA 240
 Db 181 vghtgdcmslavspdnflfsgacadasaklwdvregtcrgtqftghesdinalicffpnea 240
 QY 241 ICGSDDASCRFLDRAQELICSHESTIGCTSVAFSISGRILLAGYDFDFNCNWMDSM 300
 Db 241 ictgddascrifdiradqelictshesicgtsvafslsgrillfagydfnchnwdsi 300
 QY 301 KSERVGILSLGDHNRVSCLGVTADGMAYATGWSDSFLKWN 340
 Db 301 rservgilsghanrvsclgvtadgmavatgswdsfikwn 340

RESULT 7
 ID AAB15170 standard; Protein: 340 AA.
 AC AAB15170;
 XX DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
 XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical;
 KW mutation; mutant.
 OS Rattus sp.
 OS Synthetic.

KEY Location/Qualifiers
 FH /note= "Wild-type Lys substituted by Arg"
 FT Misc-difference 8
 XX WO20045179-A2.
 PD 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 PR 27-JAN-1999; 99US-0117404.
 PA (REGC) UNIV CALIFORNIA.
 XX PI Zuker CS, Adler JE, Lindemeier J;
 DR WPI; 2000-499361/44.
 XX PS Disclosure; Page -; 68pp; English.

The present sequence is a mutant rat G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.

Note: The present sequence is not shown in the specification but is derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see AAB15168) and information given on page 8 of the disclosure.

Sequence 340 AA;

Query Match 97.6%; score 1765; DB 21; Length 340;
 Best Local Similarity 96.8%; Pred. No. 1.2e166;
 Matches 329; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAOEQLKKQTADAKACADVTAAELVNLGVGRVQMRTRTRIGHAKYA 60
 1 mgemeqlrqeaoeqlkkqjadakaditlaelvslgvqvrqnttirighakiya 60
 Db 61 MHRATDSKLVLVASQDKLIVWDSYNTKVRHAIPLOSSWMTCAYAPSGNIVACGGIDNM 120
 QY 61 mhwatdsklvlvasdqkllivwtdyttnkvhailprsswmcayapsgnivacggidnm 120
 Db 121 CSYNLKSREGNVKVSRLSANTGILSCLRELDNNIVTSSGDTICALWDIETGGQTKV 180
 QY 121 csylnksregnkvksrelsantgylsccrelldnnivtssgdticalwdietggktvf 180
 Db 241 ICGSDDASCRFLDRAQELICSHESTIGCTSVAFSISGRILLAGYDFDFNCNWMDSM 300
 QY 241 ictgddascrifdiradqelictshesicgtsvafslsgrillfagydfnchnwdsi 300
 Db 301 KSERVGILSLGDHNRVSCLGVTADGMAYATGWSDSFLKWN 340
 QY 301 kcervgilsghanrvsclgvtadgmavatgswdsfikwn 340
 Db 301 kcervgilsghanrvsclgvtadgmavatgswdsfikwn 340

RESULT 8
 ID AAB15168 standard; Protein: 340 AA.
 AC AAB15168;
 XX DE 12-DEC-2000 (first entry)
 DE Rat; Taste Cell specific G-protein beta 3 subunit.
 XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry.
 OS Rattus sp.
 PN WO20045179-A2.
 PD 03-AUG-2000.
 XX PF 26-JAN-2000; 2000WO-US02218.
 PR 27-JAN-1999; 99US-0117404.
 XX PA (REGC) UNIV CALIFORNIA.
 PR WPI; 2000-499361/44.
 DR N-ISDB; AAY4590.
 XX PT Identifying a compound that modulates sensory signaling in sensory cells for use in pharmaceutical and food industries comprises contacting the compound with a sensory cell specific G-protein beta polypeptide -
 PT Disclosure; Page -; 68pp; English.

The present sequence is a mutant rat G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.

The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is expressed specifically in taste cells, hence this sequence is referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.

Sequence 340 AA;

referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may be used for identifying taste modulating compounds which can be used in pharmaceutical and food industries to customise taste.

Note: The present sequence is not shown in the specification but is derived from the rat wild-type TC-Gbeta3 sequence given on page 62 (see AAB15168) and information given on page 8 of the disclosure.

CC	referred to as taste cell specific G-protein beta 3 subunit (TC-Gbeta3).
CC	TC-Gbeta3 is involved in-the taste transduction pathway. TC-Gbeta3 may
CC	be used for identifying taste modulating compounds which can be used in
CC	pharmaceutical and food industries to customize taste.
CC	Note: The present sequence is not shown in the specification but is
CC	derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
CC	AB15168) and information given on page 8 of the disclosure.
XX	Sequence 340 AA;
SQ	Query Match 97.2%; Score 1759; DB 21; Length 340; Best Local Similarity 96.2%; Pred. No. 4 8e-66; Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
QY	1 MGEMEQLRQEASQKKOIAADARKACADVTAAELVSGLEVGRVQMRTRRIRGHLAKIYA 60 : : : : : : : : : : : 1 mgemeqikqeadqkqkiadarkacadtlaelvsglevygrqrtrrtirghakiya 60
DB	61 MWATDSEKLVVASQDKLIVDSYNNKVIAPLSSWVMCAVAPSGNFVACGGIDMM 120 : : : : : : : : : : 61 mwatdsklivvasqdkgkliwddtyttnkvhailplisswmtcavapsgnfvacggidm 120
QY	121 CSYLNLSREGNVKVSSELARTGTYISCCREDDNNVTTSGDTTCALWPINFTGQOKTVP 180 : : : : : : : : : 121 csiylksregnkvksrelsahtgyisccrfldnnnvtssggptcalwdeitggktvi 180
DB	181 VGHGDCLSALVSPDFNLIFSCACDASAKLMDVREGTCRQFTFGHESDIWICFPNGEA 240 : : : : : : : : 181 vghgdclsalvspdfnlifscacdasaaklmdvregtcrtfghesdiwicfpngea 240
QY	241 ICGSDASCRFLDRADOLECFSBICIGITSFASLGSRLPAGYDDNCNWMDSM 300 : : : : : : : 241 icgdsascrfldradoleltayshesicgitsvafslgsrlfagydoffnchnwdsi 300
DB	301 KSERVGILSHONRVSLGIVPAWDGMATVSGMSDFEIKIWN 340 : : : : : 301 kcervgvlgisghdnrvsclgvtaidgmavatjswsdstikwn 340
RESULT 10	
AAB15172	AAB15172 standard; Protein: 340 AA.
AC	AAC
DT	12-DEC-2000 (first entry)
XX	Mutant rat Taste Cell specific G-protein beta 3 subunit variant #3.
DE	Rat; Taste cell specific G-protein beta 3 subunit; TC-Gbeta3; taste transduction pathway; pharmaceutical; food industry; mutation; mutein; mutant.
XX	Rattus sp.
OS	Synthetic.
XX	Key Location/Qualifiers
FH	Misc-difference 191
FT	/note= "wild-type Ala substituted by Gly"
PN	WO20045179-A2.
XX	03-AUG-2000.
PD	
PP	26-JAN-2000; 2000WO-US02218.
XX	27-JAN-1999; 99US-0117404.
PA	(REGC) UNIV CALIFORNIA.
XX	Zuker CS, Adler JE, Lindemeyer J;
PI	

DR WPI; 2000-499361/44. PR 01-FEB-1994; 94US-0190802.
 XX PT (STRD) UNIV LEILAND STANFORD JUNIOR. XX
 PT PI Mochly-Rosen D, Ron D;
 PT XX DR XX
 PS XX
 XX
 CC Identifying a compound that modulates sensory signaling in sensory
 cells for use in pharmaceutical and food industries comprises
 contacting the compound with a sensory cell specific G-protein beta
 polypeptide -
 XX
 PS Disclosure; Page - ; 68pp; English.
 XX
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 beta 3 is expressed specifically in taste cells, hence this sequence is
 referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 be used for identifying taste modulating compounds which can be used in
 pharmaceutical and food industries to customize taste.
 Note: The present sequence is not shown in the specification but is
 derived from the Rat Wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 XX Sequence 340 AA;
 SQ
 Query Match 97.2%; Score 1758; DB 21; Length 340;
 Best Local Similarity 96.2%; Pred. No. 6.1e-16;
 Matches 327; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MGEMEQLRQEAFQKKQIADARKAKACDVTLAELVSGLEVVGRVQMRTRRTLGHAKIYA 60
 Db 1 ngemeqeklgqeaeqkqiqiakardakacadielavglevgrvgmrtrtlrghakiya 60
 Qy 61 MHWATDKLVSASQGKLIWDSYNTNKHAIPRSWMMTCAAPSGNIVAGGLDNM 120
 Db 61 mhwtatdklvsasqgkliwdsyntnkhaiprswwmmtcaapsgnivaggldnm 120
 Qy 121 CSYLNLSKREGNVKVSRELSAHTGTLGSSCCRPDDNNIVSSGDTTCAALDENGQKTV 180
 Db 121 csylsksregnvksrelsahtgytscrfidnnivssgdtcalwdietgqktv 180
 Qy 181 VGHTRGCMMSLAVSPRPNLFISGACASAKIWDYRGCTCROFTGHSEDINAIICFPNGEA 240
 Db 181 vghtgcmmslavsprpnlfisgacasaakiwdvrgtcrcqftghesdinaiicfpngea 240
 Qy 241 ICTGSDASERLFDRAQDLCIESHISIGGIVSFAFSGRILLAGDFDNVNWDMSM 300
 Db 241 ictgddasercldradqeqtayshiesicgivsfafsgrilfagyddfnvnwdsm 300
 Qy 301 KSERVGILSGHDNRVSLCLGVTADGAVATGSWDSFLKINN 340
 Db 301 kcergvlgshdnrvsclgvtadgavatgswwdsflkiwn 340
 RESULT 11
 AAR85859 ID AAR85859 standard; peptide; 340 AA.
 XX AC AAR85859;
 XX DT 13-SEP-1996 (first entry)
 DE WD-40 domain-contg. bovine G-beta-1 protein.
 XX
 KW WD-40 repeat region; beta-transducin; protein-protein interaction; drug;
 KW intracellular signalling; protein kinase C; homology; motif; modulator;
 receptors of activated protein kinase; enzyme activity; isozyme; human.
 OS Bos taurus.
 XX
 PN W09521252-A2.
 XX PD 10-AUG-1995.
 XX PF 31-JAN-1995; 95WO-US01210.
 XX
 PR 01-FEB-1994; 94US-0190802.
 XX PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 protein contg. a WD-40 region.
 XX Example 5; Page 102-103; 351pp; English.
 XX
 CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Protein AAR85851-92 were isolated based
 CC on homology with beta transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC AAR8585-R85862. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.
 XX Sequence 340 AA;
 SQ
 Query Match 87.2%; Score 1778; DB 16; Length 340;
 Best Local Similarity 83.2%; Pred. No. 4.2e-148;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;
 Qy 1 MGEMEQLRQEAEOLKKQIADARKAKACDVTLAELVSGLEVVGRVQMRTRRTLGHAKIYA 60
 Db 1 mseldqkrlreakeqklnqkndarkakacdatlsitnnlpvgvqmrtrtlrghakiya 60
 Qy 61 MHWATDKLVSASQGKLIWDSYNTNKHAIPRSWMMTCAAPSGNIVAGGLDNM 120
 Db 61 mhwtatdklvsasqgkliwdsyntnkhaiprswwmmtcaapsgnivaggldnm 120
 Qy 121 CSYLNLSKREGNVKVSRELSAHTGTLGSSCCRPDDNNIVSSGDTTCAALDENGQKTV 180
 Db 121 csylsksregnvksrelsahtgytscrfidnnivssgdtcalwdietgqktv 180
 Qy 181 VGHTRGCMMSLAVSPRPNLFISGACASAKIWDYRGCTCROFTGHSEDINAIICFPNGEA 240
 Db 181 tghtgcmmslavsprpnlfisgacasaakiwdvrgtcrcqftghesdinaiicfpngea 240
 Qy 241 ICTGSDASERLFDRAQDLCIESHISIGGIVSFAFSGRILLAGDFDNVNWDMSM 300
 Db 241 ictgddasercldradqeqtayshiesicgivsfafsgrilfagyddfnvnwdsm 300
 Qy 301 KSERVGILSGHDNRVSLCLGVTADGAVATGSWDSFLKINN 340
 Db 301 kadragvlgshdnrvsclgvtadgavatgswwdsflkiwn 340
 RESULT 12
 AAY67863 ID AAY67863 standard; protein; 340 AA.
 XX AC AAY67863;
 XX DT 25-APR-2000 (first entry)
 XX DE Human Rgbbl G-protein beta1 subunit amino acid sequence.
 XX KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Rgbbl;
 KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 XX G-protein coupled receptor signal transduction;

OS	Homo sapiens.	XX	10-SEP-1998 (first entry)
XX		DT	
PN	Human G-protein beta-3 subunit protein.	XX	
XX		DE	
CA2219958-A1.		XX	
PD	G-protein; beta-3 subunit; human; hypertension; immunodeficient; stroke;	XX	
XX	treatment; cardiovascular disease; metabolic disorder; tumour metastasis;	KW	
07-JUL-1999.	coronary heart disease; post-angioplasty; diabetes;	KW	
PF	nephropathy; polyneuropathy; retinopathy.	KW	
XX		XX	
XX	PR	OS	Homo sapiens.
XX	PA	XX	
(LEBE/)	LEBERER E.	PN	W09B11212-A1.
(LEEU/)	LEEUW T.	XX	
PA	(THOM/)	PD	19-MAR-1998.
PA	THOMAS D Y.	XX	
XX	(WHIT/)	PP	29-AUG-1997; 97WO-EP04709.
XX	WHITEWAY M.	XX	
PI	Leberer E, Leeuw T, Thomas DY, Whiteway M;	PR	13-SEP-1996; 96DE-1037518.
XX	DR	XX	
XX	WPI; 2000-137553/13.	PA	(SIEFF/)
XX	PT	XX	SIEFFERT W.
XX	Interacting Polypeptides involved in G-protein-coupled receptor signal	PI	Siffert W;
XX	transduction -	XX	
PS	Claim 3; Fig 6; 91pp; English.	PS	
XX		DR	WPI; 1998-271665/24.
CC	This sequence represents the beta1 subunit of a human G-protein. The	N-PSDB;	AAV34857.
CC	invention relates to the G-protein beta subunit interaction domain of the	XX	
CC	Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein	XX	
CC	kinases are p21-activated protein kinases (PAK), and they are involved in	PT	Variant of human G protein beta-3 sub-unit - associated with
CC	many varied cellular processes ranging from morphogenesis and stress	XX	hypertension
CC	response to apoptosis. Interacting polypeptides Ste4p/Gbeta and	XX	
CC	Ste20p/PAK are useful for designing in vitro and in vivo experimental	PS	Claim 2; Page 12-13; 34pp; German.
CC	models which enable the screening of large collections of synthetic,	XX	
CC	semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta	CC	This sequence represents a human G-protein beta-3 subunit consisting
CC	and Ste20p/PAK dependent diseases.	CC	of up to six WD repeat motifs (as found in normotensive subjects). The
XX	Sequence 340 AA;	CC	than the seven WD repeat motifs found in normotensive subjects). The
XX		CC	nucleic acid sequence encoding this protein can be expressed in a host
XX		CC	organism to produce the protein, preferably where the host organism is a
XX		CC	immunodeficient person, especially an HIV-positive person. This sequence
XX		CC	can be used to prepare a medicament for treating diseases associated with
XX		CC	G protein mis-control e.g. cardiovascular disease, metabolic disorders or
XX		CC	immunological diseases, hypertension, coronary heart disease, stroke,
XX		CC	post-angioplasty restenosis, diabetic complications (e.g. nephropathy, polyneuropathy or retinopathy) or tumour metastasis.
XX		CC	
PS	Query Match 87.2%; Score 1578; DB 21; Length 340;	PS	
CC	Best Local Similarity 83.2%; Pred. No. 4-2e-148;	CC	
CC	Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;	CC	
Db	1 MGEMEIQRLQEAEQQLKQIADARKACDVTLAELVSGLEVGRVQMRTRRLGHAKIYA 60	CC	
Qy	1 mselidqrlreaeqklqnqldarkacadtlsqtnnnidpvqgkliqmrttrtlghakiya 60	CC	
Qy	2 61 MHWATDKLIVSASQDGKLIWWSYTTKVKHAIPRLSSWMTCAVAYASGGNFVACGGIDNM 120	CC	
Db	1 mhwgtdsrlivsasqdgkliwdsyttnkvhailprsswmtcaayapsgnvacyggdlnm 120	CC	
Qy	3 121 CSINYLNKSREGWKVRELSAHTGYSVSCRCFLDDNNIVSSGDT'CALDIETGQQKTVF 180	CC	
Db	1 121 csiylnktrqeqnvrsvrslreahgtyscercfiddngvttsgatclwlwetggqtff 180	CC	
Qy	4 181 VGHGDCMSAVSPDFNLFLISGACDASAKLWDYREGTCRGTGHESEDINAICFPNGEA 240	CC	
Db	1 181 tghgqdmislaipdrtrlvsgadaksalwdvregmcqftghestdinaicfpngna 240	CC	
Qy	5 241 ICGSDASCRFLRADQBLICHESHESTICGITSVAFLSGLRLFAGYDDFCNVWDSM 300	CC	
Db	1 241 fatysddatcrifdradeimtysdnincigtsvsksgrlagylgddfnenwvdal 300	CC	
Qy	6 301 KSERVGLSCHDNRYNSCLGVTADGMAVGWSWDFLKWN 340	CC	
Db	1 301 kadragvlaghdnrvsclyvtddgmvavtgswdfkwn 340	CC	
RESULT 13	AAW59354	Qy	7 241 ICGSDASCRFLRADQBLICHESHESTICGITSVAFLSGLRLFAGYDDFCNVWDSM 300
ID	AAW59364	Db	8 181 VGHGDCMSAVSPDFNLFLISGACDASAKLWDYREGTCRGTGHESEDINAICFPNGEA 240
AC	AAW59364;	Qy	9 200 ictgsdascrfalradqeljcfsnesicgitsvafsa1sgrlflagyddfnenwvdsm 259

us-09-492-029-5.rag

Fri Sep 28 10:45:11 2001

PI Mochly-Rosen D, Ron D;
 XX DR WPI; 1995-28372/37.
 PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 PT protein contg. a WD-40 region.

XX Example 5; Page 109-110; 351pp; English.

XX Proteins AAR8551-82 are protein which contain at least one WD-40 (also
 CC called beta-transducin homologous) amino acid repeat motif. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR8550). Proteins AAR8551-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR8593).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85780-R8842. The peptides can be used to identify target proteins
 CC containg WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.

XX Sequence 340 AA;

SQ

Query Match 84.5%; Score 1528; DB 16; Length 340;
 Best Local Similarity 80.9%; Pred. No. 3; 8e-143; Indels 0; Gaps 0;
 Matches 275; Conservative 31; Mismatches 34; Indels 0;

QY 1 MCEMEQLOREAEOLKKQIADARKACADVTLASLVSLEVVGRVQMPTRRTLRGHAKIYA 60
 Db 1 mseliedqirgeeqelqninqardarkacqdstltqtagldpvgriqntrrlrgplakiya 60

QY 61 MRWATDSKLLVYASQDGKLIVWDWSYTINRVAHAPLRSWWMTCAYARSGNEVAGCGIDM 120
 Db 61 mwngtdsrlivrasqgkliiwdsyttnkvhaiprlsswmmtcaypsgnvacggldni 120

QY 121 CSTVNLKREGKVKVSRELSAHTGLSCRFDDNNIVTSSGTTCALWDIEFQOKTVF 180
 Db 121 cslysktrgnyrvsrelphtgysccrfddqitssgttcalwdiegqtvgf 180

QY 181 VGHGTGDCMSLAVNSPDFFNLIFISACDASAKLWDVREGTCQTFCHESDINAICFFPNEA 240
 Db 181 aghsgdavmslalpdgrifvsacdasiklwdrismcrqtfghesdinavrafpgya 240

QY 241 ICTGSDASDRFLDRADDELCEFLCSHHSIIGCTSAFSISGRULFAGYDDFFCNVWDSM 300
 Db 241 fctgsdattciflradqelmyshdnlicgitsvafsafrsgrillagydffnoinwdam 300

QY 301 KSERVTEILSGHDNRVSLCLGVITADGMAVTGSDNSELWN 340
 Db 301 kgdrayvlagdnrvsclytdggmavtgswsfklwn 340

Search completed: September 28, 2001, 10:29:22
 Job time: 72 sec

GenCore version 4.5						
Copyright (c) 1993 - 2000 Compugen Ltd.						
OM protein - protein search, using sw model						
Run on: September 28, 2001, 10:28:39 ; Search time 20.71 Seconds						(without alignments)
Scoring table: BLOSUM62						338.036 Million cell updates/sec
Searched: 197339 seqs, 20590346 residues	Gapop 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters:	197339					
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
Database :	Issued_Patents_AA,*					
1:	/cgn2_6/potodata/2/1aa/5A.COMB.pep:*					
2:	/cgn2_6/potodata/2/1aa/5B.COMB.pep:*					
3:	/cgn2_6/potodata/2/1aa/6A.COMB.pep:*					
4:	/cgn2_6/potodata/2/1aa/6B.COMB.pep:*					
5:	/cgn2_6/potodata/2/1aa/pctrus.COMB.pep:*					
6:	/cgn2_6/potodata/2/1aa/backfile1.pep:*					
Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Length	DB ID	Description		
1	1809	10.0	340	4 US-09-180-783-2	Sequence 2, Appli	
2	1578	87.2	340	1 US-08-190-802A-38	Sequence 38, Appli	
3	1558.5	86.2	299	4 US-07-147-826-2	Sequence 2, Appli	
4	1528	84.5	340	1 US-08-190-802A-42	Sequence 42, Appli	
5	1463	80.9	341	1 US-08-190-802A-45	Sequence 45, Appli	
6	1459	80.7	340	1 US-08-190-802A-40	Sequence 39, Appli	
7	1421	78.6	326	1 US-09-190-802A-39	Sequence 1, Appli	
8	949.5	52.5	395	3 US-09-032-372-1	Sequence 61, Appli	
9	650	35.9	423	1 US-08-190-802A-61	Sequence 27, Appli	
10	305.5	16.9	317	1 US-08-190-802A-27	Sequence 41, Appli	
11	305.5	16.9	317	1 US-08-190-802A-41	Sequence 47, Appli	
12	205.6	16.9	704	1 US-08-190-802A-62	Sequence 62, Appli	
13	296	16.4	704	1 US-08-188-502-5	Sequence 5, Appli	
14	296	16.4	704	1 US-08-188-502-5	Sequence 5, Appli	
15	296	16.4	704	1 US-08-164-715-5	Sequence 27, Appli	
16	296	16.4	704	2 US-08-308-818-3	Sequence 41, Appli	
17	287	15.9	587	3 US-08-899-578-2	Sequence 47, Appli	
18	274	15.1	704	1 US-08-582-18	Sequence 18, Appli	
19	274	15.1	704	1 US-08-546-715-18	Sequence 18, Appli	
20	271.5	15.0	439	1 US-08-190-802A-65	Sequence 65, Appli	
21	271.5	14.6	318	1 US-08-150-802A-33	Sequence 33, Appli	
22	257.5	14.2	514	1 US-08-190-802A-66	Sequence 66, Appli	
23	251	13.9	798	1 US-08-190-802A-64	Sequence 64, Appli	
24	251	13.9	798	1 US-08-190-802A-68	Sequence 68, Appli	
25	251	13.9	798	2 US-08-308-818-2	Sequence 2, Appli	
26	247	13.7	713	1 US-08-190-802A-63	Sequence 63, Appli	
27	13.4	375	4	US-08-063-743-1	Sequence 1, Appli	

SUMMARIES

RESULT 1
US-09-180-783-2
; Sequence 2, Application US/09180783
; Sequence 1, Application US-09-180-783-2
; Patent No. 6242181

GENERAL INFORMATION:

APPLICANT: Siffrert, Winfried
TITLE OF INVENTION: THE USE OF A GENETIC MODIFICATION IN THE GENE FOR HUMAN PROTEIN b3 SUBUNIT FOR THE DIAGNOSIS OF DISEASES

FILE REFERENCE: 1135-2

CURRENT APPLICATION NUMBER: US/09/180_783

CURRENT FILING DATE: 1999-03-17

PRIOR APPLICATION NUMBER: PCT/EP97/02250

PRIOR FILING DATE: 1997-05-02

PRIOR APPLICATION NUMBER: DE 19619362.1

PRIOR FILING DATE: 1996-05-14

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 2

LENGTH: 340

TYPE: PRT

ORGANISM: HOMO sapiens

US-09-180-783-2

Db 301 KSERVGLSCLGVTDGMATGSWDSFLKINN 340

RESULT 2

US-08-190-802A-38

; Sequence 36, Application US/08190802A

PATENT NO. 551003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 334-0960

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: G-Beta 1 bovine, FIG. 21

US-08-190-802A-38

Qy 301 KSERVGLSCLGVTDGMATGSWDSFLKINN 340

Db 301 KADRGAVLGLHDNRVSCLGVTADGMATGSWDSFLKINN 340

RESULT 3

US-09-147-826B-2

; Sequence 2, Application US/09147826B

; Patent No. 6255853

GENERAL INFORMATION:

APPLICANT: Siffert, Winfried

TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE

FILE REFERENCE: 1135-003

CURRENT APPLICATION NUMBER: US/09/147,826B

CURRENT FILING DATE: 1999-03-15

PRIORITY APPLICATION NUMBER: PCT/EP97/04709

PRIORITY FILING DATE: 1997-08-29

PRIORITY APPLICATION NUMBER: DE 196 37 518.5

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 299

TYPE: RTT

ORGANISM: Homo sapiens

US-09-147-826B-2

Query Match Best Local Similarity 86.2%; Score 1558.5; DB 4; length 299; Matches 299; Conservative 0; Mismatches 0; Indels 41; Gaps 1;

Qy 1 MGEMEQLQEAEQLKKQIAADARKACADVTIAELVSGLEVGRYQMRRTTLRGHLAKYA 60

Db 1 MGEMEQLQEAEQLKKQIAADARKACADVTIAELVSGLEVGRYQMRRTTLRGHLAKYA 60

Qy 61 MWATDKSLVYASODGKLTVWDSYTNTKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120

Db 61 MWATDKSLVYASODGKLTVWDSYTNTKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120

Qy 121 CSIYNLKSREGNVKVSRELSAHTHGVLSCRFEDDNNTVSGDTICLALWQIET-QQKVF 180

Db 121 CSIYNLKSREGNVKVSRELSAHTHGVLSCRFEDDNNTVSGDTICLALWQIET-QQKVF 180

Qy 181 VGHGDMSLAVSPDFNLIFISGACDASAKLWQWREGTCROFTGHSEDINAICFPNEA 240

Db 167 -----AKLWQWREGTCROFTGHSEDINAICFPNEA 166

Qy 241 ICGSDDASCRFLDRAQELICFSHSITCGITSAFSLSGRILFAGYDDFNCONVNDSM 300

Db 200 ICGSDDASCRFLDRAQELICFSHSITCGITSAFSLSGRILFAGYDDFNCONVNDSM 259

Qy 301 KSERVGLSCLGVTDGMATGSWDSFLKINN 340

Db 260 KSERVGLSCLGVTDGMATGSWDSFLKINN 299

RESULT 4

US-08-190-802A-42

; Sequence 42, Application US/08190802A

; Patent No. 551003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: G-Beta 2 (Human), Fig. 25

US-08-190-802A-42

Query Match 84.5%; Score 1528; DB 1; Length 340;
Best Local Similarity 80.9%; Pred. No. 1.1e-143; Indels 0; Gaps 0; Matches 275; Conservative 31; Mismatches 34;

Query 1 MGEMEQLRQEAEQKKQIAARKAKADVTIAELVSGLEVLGVGRYOMTRTRLGLHLAKIYA 60

Db 1 MSEBLQLRQEAEQKKQIAARKAKADVTIAELVSGLEVLGVGRYOMTRTRLGLHLAKIYA 60

Query 61 MWATDKSLVLSASQDGLKLIWDSYTNTKHAIPRSWMTCAVAPSGNFVACGGIDN 120

Db 61 MWHTGDSRLVLSASQDGLKLIWDSYTNTKHAIPRSWMTCAVAPSGNFVACGGIDN 120

Query 121 CSTYLNLSREGANVKVSRELSAHTGVLSCCRPLDDNNIVTSSGDTTCALMDIETGQKTVF 180

Db 121 CSHYSLKTREGNVYRSELPEHGTGVLSCCRFLDDNQITSSGDTTCALMDIETGQTVFG 180

Query 181 VGMGDCMSLAVSPDNFLNFTSGACASAKLMDVRECTCROFTGHESDINAICFPNGEA 240

Db 181 AGHSDGVMISLAPDGKTFVNSACASAKLMDVRCOTFHESDINAICFPNGEA 240

Query 241 ICGSDDASCRFLDRADQELICFSHESITCGITSAFLSGRLIFAGYDDFNCDNWDSM 300

Db 241 FTGSDDATCRFLDRADQELIMSHDNIIGGITSVAFSRSGRLLAGVDFNCNWIDAM 300

Query 301 KSERVGILSGHDNRVSVCLGVTADGMAVATGSWDSFLKIWN 340

Db 301 KGDRAGVLAGHDNRVSVCLGVTDDGMAVATGSWDSFLKIWN 340

RESULT 5

US-08-190-802A-45

Sequence 45 Application US/08190802A

Patient No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA
COUNTY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 341 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28

US-08-190-802A-45

Query Match 80.9%; Score 1463; DB 1; Length 341;
Best Local Similarity 79.0%; Pred. No. 3e-137; Indels 0; Gaps 0; Matches 267; Conservative 32; Mismatches 39;

Query 3 ENEQOLQEABQKKQIAARKAKADVTIAELVSGLEVLGVGRYOMTRTRLGLHLAKIYAH 62

Db 4 EELAQEOEQEOKNOIREKARRKAADTTLAMATANVEPGVGRYOMTRTRLGLHLAKIYAH 63

Query 63 WATDKSLVLSASQDGLKLIWDSYTNTKHAIPRSWMTCAVAPSGNFVACGGIDN 122

Db 64 WASDRMIVLSASQDGLKLIWDSYTNTKHAIPRSWMTCAVAPSGNFVACGGIDN 123

Query 123 IYNLKSREGANVKVSRELSAHTGVLSCCRPLDDNNIVTSSGDTTCALMDIETGQKTVF 182

Db 124 IYSIKTREGNVYRSELPEHGTGVLSCCRFLDDNQITSSGDTTCALMDIETGQTVFG 183

Query 183 HEDCMISLAVSPDNFLNFTSGACASAKLMDVRECTCROFTGHESDINAICFPNGEA 242

Db 184 HGDYVMSLAPDMRPTFVNSACASAKLMDVRCOTFHESDINAICFPNGEA 243

Query 243 TGSDDASCRFLDRADQELICFSHESITCGITSAFLSGRLIFAGYDDFNCDNWDSM 302

Db 244 TGSDDATCRFLDRADQELIMSHDNIIGGITSVAFSRSGRLLAGVDFNCNWIDAM 303

Query 303 ERVGLGILSGHDNRVSVCLGVTADGMAVATGSWDSFLKIWN 340

Db 304 ERAGVLAGHDNRVSVCLGVTDDGMAVATGSWDSFLKIWN 341

ZIP: 94306-0850
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 341 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28

RESULT 5

US-08-190-802A-40

Sequence 40 Application US/08190802A

Patient No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEX: (415) 324-0880
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 340 amino acids
 TYPE: amino acid
 TOPOLogy: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G- BETA DROSOPH. Fig. 23
 US-08-190-802A-40

Query Match Similarity 80.7%; Score 1459; DB 1; Length 340;
 Best Local Similarity 77.4%; Pred. No. 7.6e-17;
 Matches 263; Conservative 35; Mismatches 42; Indels 0; Gaps 0;
 QY 1 MGEMRSQRLRQAERQKQIADARKACADYVLAELVSGLEVGRVQMRRTLRGHAKIYA 60
 Db 1 MNELDSLRQRAESKNAIRDAKACDTSILQATSLSPPIGRQMRTRTRLGHAKIYA 60
 QY 61 MHWAUDSKLVLSSAQDGKLIWVWYSSYTNNVHAIPRLRSSWMTCAYAPSGNFWAGGLDNM 120
 Db 61 MHWGNDNSRNLYSASQDGKLIWVSHHTNNVHAIPRLRSSWMTCAYAPSGNFWAGGLDNM 120
 QY 121 CSINKLKSREGNVYKVSRLESAHGTGQLSCRFEDDDNTVTTSSCDTCAALWDITETGQKTVF 180
 Db 121 CSINKLKSREGNVYKVSRLESAHGTGQLSCRFEDDDNTVTTSSCDTCAALWDITETGQKTVF 180
 QY 181 VGHGDCMSLAVBDNFNLPTISGACDASAKLWVREGCROPTGHSEDINAICFPNGEA 240
 Db 181 LGHGDVMSLARPOCKIFVSGRADASAKLWDIREGVCKOTFPGHESDINAVTFPPNGQA 240
 QY 241 ICTOSDDASCRLLTQAOELICFHESIICITSYAFLSISGRLLAEAGYDFNCWDFSM 300
 Db 241 FAFGSDATCRLFDIRQDQELAMYSHDNIICITSYAFLSISGRLLAEAGYDFNCWDFSM 300
 QY 301 KSEVGVLSGHDNRVSCIGVYTAGDGMATGSMDSFLKIWN 340
 Db 301 KAEGSGLLAGHDNRVSCIGVYTAGDGMATGSMDSFLKIWN 340
 RESULT 7
 US-08-190-802A-39

Sequence 39 Application US/08190802A
 Patent No. 515903

GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and uses
 NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Denlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEX: (415) 324-0880
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 TOPOLogy: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G-beta - bovine (2), Fig. 22
 US-08-190-802A-39

Query Match Similarity 78.6%; Score 1421; DB 1; Length 326;
 Best Local Similarity 78.2%; Pred. No. 4.2e-13;
 Matches 259; Conservative 29; Mismatches 33; Indels 10; Gaps 2;
 QY 15 KQJADARKACADYVLAELVSGLEVGRVQMRRTLRGHAKIYAMHWATDSKLVLSS 74
 Db 1 RQNQIRDARKACGHSITLQTITASLDPVGRIQMRTRTRLGHAKIYAMHWGTDSSLVVA 60
 QY 75 ODKLILWDS---YTNKVKAIPLRSSWMTCAYAPSGNFWAGGLDNMCSTYLNKR 129
 Db 61 ODKLILWDS---YTNKVKAIPLRSSWMTCAYAPSGNFWAGGLDNMCSTYLNKR 120
 QY 130 EGNYKVSRBLASTGTYLSCRFEDDDNTVTTSSCDTCAALWDITETGQKTVFVHGDCMS 189
 Db 121 ---VSRELPQHNGYLSCRCRFLDDNTVTTSSCDTCAALWDITETGQKTVFVHGDS 175
 QY 190 LAVSPDNEFLPTISGACDASAKLWDIREGTCTGHSEDINAICFPNGEBAICGSDDS 249
 Db 176 LSLPDGRTFVSGACDASIKLWDVRUSMCRQFTGHSEDINAIAVFFPNTYAFITGSDDAT 235
 QY 250 CRFLDFLRADQEJCFSHESIICITSYAFLSISGRLLAEAGYDFNCWDFSM 309
 Db 236 CRFLDFLRADQEJCFSHESIICITSYAFLSISGRLLAEAGYDFNCWDFSM 295
 QY 310 GHDRVSCIGVYTAGDGMATGSMDSFLKIWN 340
 Db 296 GHDRVSCIGVYTAGDGMATGSMDSFLKIWN 326
 RESULT 8
 US-09-032-372-1
 Sequence 1 Application US/0903237
 Patent No. 600837
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032,372
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0478 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX:
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 395 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB01
 CLONE: 78191
 09-032-372-1

QY 318 LGVTDGMAVATGSMDSFLKTN 340
 US-08-190-802A-27
 Sequence 27, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 TITLE OF INVENTION: WD-40 - Derived Peptides and uses
 NUMBER OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEX/FAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: RACK1 amino Acid Sequence, Fig. 1C
 US-08-190-802A-27

Query Match 16.9%; Score 305.5; DB 1; Length 317;
 Best Local Similarity 31.5%; Pred. No. 2.2e-22;
 Matches 82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;
 QY 48 RPLRLGHAKITAMHAWTDLSKILVSASODGLKLVWMSYTNTKVHAIPRSSLWYSWTMCAYP 107
 DB 56 QRALRGHSFHVSDVVTSSDGFALSGSWDGTLRMLDTGTTTRRFVGHTKDVLSVAFSS 115
 QY 108 SGNFVAACGGLDNMCSITYNLKSREGNVKVRSELSAHTGYLSCCREL--DDNNIVTSSG-DT 164
 DB 116 DNQTVSGSRDKTIKWNLT--GVCKTYWQDESHSEWWSCVRFSPNSNPITVSCGWDK 172
 QY 165 TCAALWIDETGQOKTVFGHGDCKMSILAVSPDFNIFISGACDASKLMDVREGTCRQFTG 224
 DB 173 LVKVVWLNANCLKTNIGHGTYLNLVTVSPDGSLLCAGSGKDGQMLWDLNNEGRHLVLDG 232
 QY 225 HESDINAICFPNGRAICGSDSDDASCRDIDRA-----DQELICSHESITCGITSA 277
 DB 233 GDI-INALCFSPNRYWLCAAT-GPSIKIWLDESKIKIVDELKEVISTSSKAEPPQCTSLA 290
 QY 278 FSLSGRLLFAGYDDEPCNW 297
 DB 291 WSADQOTLFLAGYNTNLVRW 310

RESULT 12

US-08-190-802A-47

Sequence 47, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

US-08-190-802A-47

RESULT 13

US-08-190-802A-62

Sequence 62, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TIF, Fig. 45

US-08-190-802A-62

RESULT 14

US-08-190-802A-63

Sequence 63, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

US-08-190-802A-47

RESULT 15

US-08-190-802A-64

Sequence 64, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

US-08-190-802A-47

RESULT 16

US-08-190-802A-65

Sequence 65, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

US-08-190-802A-47

RESULT 17

US-08-190-802A-66

Sequence 66, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

US-08-190-802A-47

RESULT 18

US-08-190-802A-67

Sequence 67, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

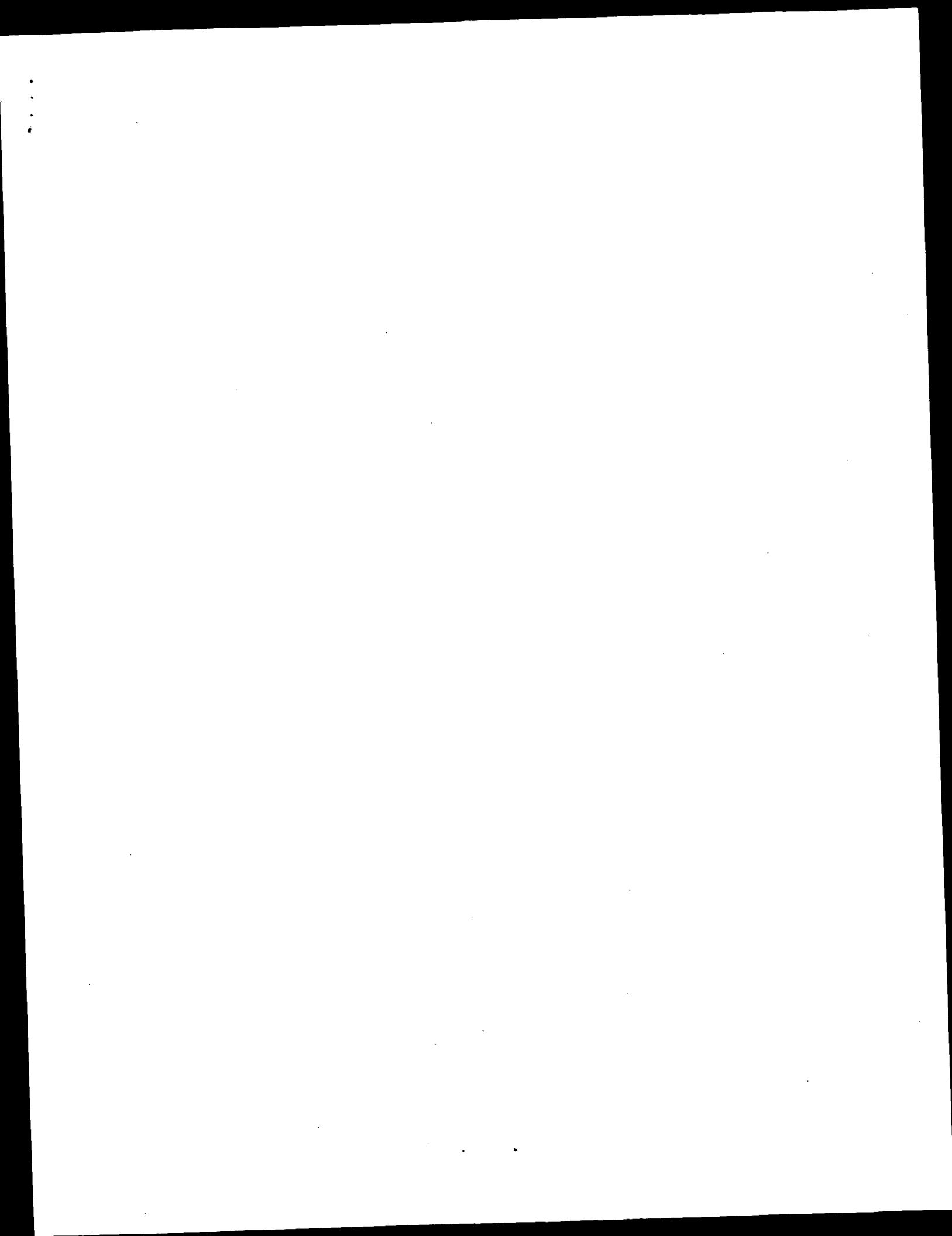
ORIGINAL SOURCE:

Fri Sep 28 10:45:11 2001

us-09-492-029-5.Fai

QY	206	ASAKLMDVREGTCTQFTGHESDINAICFFPNEAICTGSDASCRFLDLRAOEL-TCF	513
Db	514	SHESTICGITSVAFSLSGRLLEAGYDDFNCCWWDMSKSERVGTLSGHDRNVCCLGVADG	573
QY	265	574 GHKG--SVSISLAFAACGCGTTLASGSVDHNITIWLDSNSLVTILURHTSTVITIFSRDG	324
QY	325	631 TVLAAAGLDNNLTFLWD	630
Db			

Search completed: September 28, 2001, 10:28:40
Job time: 31 sec



GenCore version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

run on: September 28, 2001, 10:33:20 ; search time 25.94 Seconds
(without alignments)
Sequence: 1 MGEEMEQIRQEAEQLKKQIAD.....TAGDMAVATGSDWSFLKINN 340
998.433 Million cell updates/sec

Scoring table: BLOSUM62
GapOp 10.0 , gapext: 0.5

Searched: 219241 seqs, 76174552 residues

total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match Length	DB ID	Description
1	1809	100.0	RGHUB3	GTP-binding regula
2	1762	97.4	340	G protein beti-sub
3	1578	87.2	340	GTP-binding regula
4	1578	87.2	340	GTP-binding regula
5	1528	87.2	340	G protein beta 1 -
6	1525	84.5	340	GTP-binding regula
7	1520	84.3	340	GTP-binding regula
8	1500	82.9	340	GTP-binding regula
9	1480	81.8	341	GTP-binding regula
10	1469	81.2	326	GTP-binding regula
11	1463	80.9	341	GTP-binding regula
12	1459	80.7	340	GTP-binding regula
13	1459	80.7	1 RGFBBH	GTP-binding regula
14	1238	68.4	A47370	GTP-binding regula
15	948.5	52.4	353	A45495 GTP-binding beta-5 GTP-binding
16	927.5	51.3	356	GTP-binding regula
17	847	46.8	380	GTP-binding regula
18	831	45.9	2 T02085	GTP-binding regula
19	824	45.6	2 T04086	GTP-binding protei
20	822	45.4	2 T03256	GTP-binding protei
21	822	45.4	2 T07376	G-protein beta cha
22	822	45.4	2 T04089	GTP-binding protei
23	821	45.4	1 RGFBB	GTP-binding regula
24	815	45.1	2 T05266	GTP-binding regula
25	794	43.9	2 T08036	GTP-binding regula
26	790	43.7	2 T16985	GTP-binding protei
27	743.5	41.1	2 T17256	GTP-binding protei
28	670	31.7	2 S7274	GTP-binding regula
29	668	36.9	2 T50474	GTP-binding regula

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS	
RESULT	1
R	RGHB3
GTP-binding regulatory protein beta-3 chain - human	beta-3 chain; heterotrimeric N
N	Alternate names: guanine nucleotide binding protein beta-3 chain; heterotrimeric GTP-binding protein
C	Species: Homo sapiens (man)
C	#sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C	Date: 31-Dec-1992
C	Accession: A35096
R	Levine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.
P	Proc. Natl. Acad. Sci. U.S.A. 87, 2329-2333, 1990
A	Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-sul
A	41 305.5 16.9 502 2 T41148
A	42 300.5 16.6 586 2 T38992
A	43 299.5 16.6 1693 2 S76056
A	44 299 16.5 1049 2 T42045
A	45 297 16.4 554 2 T02445
R	Accession: A35096
A	Molecule type: mRNA
A	Residues: 1-340 <LEV>
A	Cross-references: GDB:120005; OMIM:139130
A	Map position: 12p13-12p13
C	Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C	Keywords: GTP-binding; heterotrimer; signal transduction
F	;51-84;/domain: WD repeat homology <WD1>
F	;88-126;/domain: WD repeat homology <WD2>
F	;139-171;/domain: WD repeat homology <WD3>
F	;180-213;/domain: WD repeat homology <WD4>
F	;222-255;/domain: WD repeat homology <WD5>
F	;233-299;/domain: WD repeat homology <WD6>
F	;308-340;/domain: WD repeat homology <WD7>
R	Comment: The G proteins are a family of guanine nucleotide-binding proteins that appear to be common. The beta and gamma chains, required for GTPase activity, are specific for each type of G protein. It is specific for each type of G protein.
C	Comment: In mammals, four distinct types of beta chains have been found.
C	Genetics:
A	Gene: GDB:GNB3
A	Cross-references: GDB:120005; OMIM:139130
A	Map position: 12p13-12p13
C	Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C	Keywords: GTP-binding; heterotrimer; signal transduction
F	;51-84;/domain: WD repeat homology <WD1>
F	;88-126;/domain: WD repeat homology <WD2>
F	;139-171;/domain: WD repeat homology <WD3>
F	;180-213;/domain: WD repeat homology <WD4>
F	;222-255;/domain: WD repeat homology <WD5>
F	;233-299;/domain: WD repeat homology <WD6>
F	;308-340;/domain: WD repeat homology <WD7>
R	Query Match 100.0%; Score 1809; DB 1; Length 340;
R	Best Local Similarity 100.0%; Pred. No. 7.5e-45; Indels 0; Gaps 0;
R	Matches 340; Conservative 0; Mismatches 0; Gaps 0;
Oy	1 MGEMEOLRQRAEOLKKQIADARKACADVTLAELVSGLEVGNGVRGVOMRTTRTGLHLKIYA 60
Oy	1 MGEMEOLRQRAEOLKKQIADARKACADVTLAELVSGLEVGNGVRGVOMRTTRTGLHLKIYA 60
Db	1 MGEMEOLRQRAEOLKKQIADARKACADVTLAELVSGLEVGNGVRGVOMRTTRTGLHLKIYA 60
Qy	61 MWATOSKLVVASQDGKLTVWDSYTNNKHAIPRSSWMTCAYAPSQGNFVACGGIDNM 120
Db	61 MWATOSKLVVASQDGKLTVWDSYTNNKHAIPRSSWMTCAYAPSQGNFVACGGIDNM 120
Qy	61 MWATDSKLVLVSASQDGKLTVWDSYTNNKHAIPRSSWMTCAYAPSQGNFVACGGIDNM 120
Db	61 MWATDSKLVLVSASQDGKLTVWDSYTNNKHAIPRSSWMTCAYAPSQGNFVACGGIDNM 120
Qy	121 CSYLNLSREGKVKSSELSAHTGVLSCCFLDDNNIVSSGDPITCALMDIEGTQKTVF 180
Db	121 CSYLNLSREGKVKSSELSAHTGVLSCCFLDDNNIVSSGDPITCALMDIEGTQKTVF 180
Qy	181 VGHGDCMSLAVSPDNEULFTSACDASAKLMDVREGTCRQTFTGHSIDNIAICFPNGEA 240

	Matches	Conservative	32;	Mismatches	25;	Indels	0;	Gaps	0;	
A;Cross-references: GB:M13236; NID:9163782; PID:9163783	Qy	1	MGEMLQRLRQEADLQLKQTADARKACADYLAEVLNSGLEVRQMRTRTRLGHAKIYA	60	Oy	1	MGEMLQRLRQEADLQLKQTADARKACADYLAEVLNSGLEVRQMRTRTRLGHAKIYA	60	C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay signals. The beta and gamma chains, required for GTPase activity, appear to be common to all	
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	Db	1	MSELDQQLRQEADLQLKQTADARKACADYLAEVLNSGLEVRQMRTRTRLGHAKIYA	60	Qy	61	MHWATDSKLIVSASODGKLIWMSYTNTKVAIPLRSSWVMTCAVAPSGNVAACGGIDNM	120	C;Keywords: GTP-binding; heterotrimer; signal transduction	
F;51-84/Domain: WD repeat homology <WD1>	Db	61	MHWATDSKLIVSASODGKLIWMSYTNTKVAIPLRSSWVMTCAVAPSGNVAACGGIDNM	120	Qy	61	MHWATDSKLIVSASODGKLIWMSYTNTKVAIPLRSSWVMTCAVAPSGNVAACGGIDNM	120	F;88-126/Domain: WD repeat homology <WD2>	
F;139-171/Domain: WD repeat homology <WD3>	Db	121	CSIYNUKSRGNGVVKVSRELSAHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	Qy	121	CSIYNUKSRGNGVVKVSRELSAHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	F;180-213/Domain: WD repeat homology <WD4>	
F;222-255/Domain: WD repeat homology <WD5>	Db	121	CSIYNUKTRBGNVRSRELAGHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	Qy	121	CSIYNUKTRBGNVRSRELAGHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	F;263-299/Domain: WD repeat homology <WD6>	
F;308-340/Domain: WD repeat homology <WD7>	Db	181	TGHTGDVMSLISLAPDTRLFGVSGACDASAKLWDREGMCROTGFHESDINAICFFNGNA	240	Qy	181	VGHTGDVMSLISLAPDTRLFGVSGACDASAKLWDREGMCROTGFHESDINAICFFNGNA	240	Qy	
Query Match	87.2%; Score 1578; DB 1; Length 340; Best local Similarity 83.2%; Pred. No. 2.1e-125; Mismatches 25; Indels 0; Gaps 0; Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;	Qy	241	ICTGSDASCRFLDRADQELCISHESTICGTSVAFSLGRLLFAGYDPFCNTWDSM	300	Qy	241	ICTGSDASCRFLDRADQELCISHESTICGTSVAFSLGRLLFAGYDPFCNTWDSM	300	Db
Best Local Similarity 83.2%; Pred. No. 2.1e-125; Mismatches 25; Indels 0; Gaps 0; Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;	Db	241	FATGSDATCFLDFLDRADQELCISHESTICGTSVAFSLGRLLFAGYDPFCNTWDSM	300	Qy	301	KSERVGLTGHIDNRVSLCLGVTADGMAVATGSWSDFLKWN	340	Qy	
Qy	61	MHWATDSKLIVSASODGKLIWMSYTNTKVAIPLRSSWVMTCAVAPSGNVAACGGIDNM	120	Db	301	KADRAGVLAGHNDNRSVCLGVTDGMAVATGSWSDFLKWN	340	Db		
Db	61	MHWATDSKLIVSASODGKLIWMSYTNTKVAIPLRSSWVMTCAVAPSGNVAACGGIDNM	120	RESULT	6	RGRHB2	GTB-binding regulatory protein beta-2 chain - human	N;Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-protein	R;Species: Homo sapiens (man)	
Qy	121	CSIYNUKSRGNGVVKVSRELSAHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	C;Date:	31-Dec-1992	#sequence_revision	31-Dec-1992 #text_change	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Accession: B26617	
Db	121	CSIYNUKSRGNGVVKVSRELSAHTGYLSCRCFLDDNNNTTSSGDTTCALWDTEGQOKTVF	180	C;Accession:	B26617	#sequence_revision	31-Dec-1992 #text_change	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	R;Fong, H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.	
Qy	181	VGHTGDVMSLISLAPDTRLFGVSGACDASAKLWDREGMCROTGFHESDINAICFFNGNA	240	Proc:	Natl. Acad. Sci. U.S.A.	84,	3792-3796,	1987	Proc:	
Db	181	TGHTGDVMSLISLAPDTRLFGVSGACDASAKLWDREGMCROTGFHESDINAICFFNGNA	240	A;Title:	Distinct forms of the beta subunit of GTP-binding regulatory proteins identified by immunological cross-reactivity	A;Title:	31-Jan-1997 #sequence_revision	A;Title:	R;Gao, B.; Gilman, A.G.; Robishaw, J.D.	
Qy	241	ICTGSDASCRFLDRADQELCISHESTICGTSVAFSLGRLLFAGYDPFCNTWDSM	300	A;Reference number:	A94155; MUID:87231903	A;Reference number:	31-Jan-1997 #sequence_revision	A;Reference number:	P;Robishaw, J.D.; Gilman, A.G.	
Db	241	FACTSDATCFLDFLDRADQELCISHESTICGTSVAFSLGRLLFAGYDPFCNTWDSM	300	A;Accession:	B26617	A;Accession:	31-Jan-1997 #sequence_revision	A;Accession:	P;Robishaw, J.D.; Gilman, A.G.	
Qy	301	KSERVGLTGHIDNRVSLCLGVTADGMAVATGSWSDFLKWN	340	A;Molecule type:	mRNA	A;Molecule type:	31-Jan-1997 #sequence_revision	A;Molecule type:	R;Gao, B.; Gilman, A.G.; Robishaw, J.D.	
Db	301	KADRAGVLAGHNDNRSVCLGVTDGMAVATGSWSDFLKWN	340	A;Residues:	1-340 <FON>	A;Residues:	31-Jan-1997 #sequence_revision	A;Residues:	P;Robishaw, J.D.; Gilman, A.G.	
RESULT	5	JC5057	G protein beta 1 - mouse	A;Cross-references: GB:M16514; MID:9183469; PID:AAA03179.1; PID:9386751	A;Cross-references:	GB:M16514; MID:9183469; PID:AAA03179.1; PID:9386751	A;Cross-references:	GB:M16514; MID:9183469; PID:AAA03179.1; PID:9386751	A;Cross-references:	
G protein beta 1 - mouse	C;Species:	Mus musculus (house mouse)	C;Species:	Mus musculus (house mouse)	C;Species:	Mus musculus (house mouse)	C;Species:	Mus musculus (house mouse)	C;Species:	
C;Date:	31-Jan-1997 #sequence_revision	31-Jan-1997 #text_change	C;Date:	31-Jan-1997 #sequence_revision	C;Date:	31-Jan-1997 #text_change	C;Date:	31-Jan-1997 #sequence_revision	C;Date:	
C;Accession:	JC5057		C;Accession:	JC5057	C;Accession:	JC5057	C;Accession:	JC5057	C;Accession:	
R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.		R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	R;Oiu, R.; Schimmer, B.P.	
Gene 175, 275-277, 1996	Gene 175, 275-277, 1996		Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	Gene 175, 275-277, 1996	
A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	A;Title: CDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins for G protein beta 1 - mouse	
A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	A;Reference number: JC5057; MUID:91707464	
A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	A;Accession:	
A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	
A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	A;Residues: 1-340 <Q0U>	
A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	A;Cross-references: GB:U29055; NID:9868168; PIDN: AAC52905.1; PID:9868169	
A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	A;Experimental source: adrenal glands	
C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	C;Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory protein beta chain; WD repeat homology	
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology	
F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	F;51-84/Domain: WD repeat homology <WD1>	
F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	F;139-171/Domain: WD repeat homology <WD2>	
F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	F;180-213/Domain: WD repeat homology <WD3>	
F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	F;188-226/Domain: WD repeat homology <WD4>	
F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	F;222-255/Domain: WD repeat homology <WD5>	
F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	F;263-299/Domain: WD repeat homology <WD6>	
F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	F;308-340/Domain: WD repeat homology <WD7>	
Query Match	87.2%; Score 1578; DB 1; Length 340; Best local Similarity 83.2%; Pred. No. 2.1e-125; Mismatches 25; Indels 0; Gaps 0; Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;	Query Match	84.5%; Score 1528; DB 1; Length 340; Best local Similarity 80.9%; Pred. No. 3.5e-121; Mismatches 34; Indels 0; Gaps 0; Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;							

A;Title: diversity among the beta subunits of heterotrimeric GTP-binding proteins: chara
A;Reference number: JS0669; MUID:92181467
A;Accession: JS0669
A;Molecule type: mRNA
A;Residues: 1-140 <VON>
C;Cross-references: GB:566124; NIDN:RAB21609_1; PID:9246470
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
rare; it is specific for each type of G protein.

C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C;Keywords: GTP binding; heterotrimer; signal transduction
F;51-84/Domain: WD repeat homology <WD1>
F;88-126/Domain: WD repeat homology <WD2>
F;139-171/Domain: WD repeat homology <WD3>
F;180-213/Domain: WD repeat homology <WD4>
F;222-255/Domain: WD repeat homology <WD5>
F;263-299/Domain: WD repeat homology <WD6>
F;308-340/Domain: WD repeat homology <WD7>

Query Match 82.9%; Score 1500; DB 1; Length 340;

Best Local Similarity 78.8%; Pred. No. 8e-119; Matches 268; Conservative 38; Mismatches 34; Indels 0; Gaps 0; C;Accession: YN1KSREGNVSKSRELSAHTSYLSCCREFLDDNNIVSGDTCAALWDETGQQKVYFG 182
Qy 1 MGEEMEOLRQEAEOLKKQIADARKACADVTIAELVSLLEVYGRVQMRTRRLGHAKIYA 60
Db 1 MSELEOLRQEAEOLKKQIADARKACADVTIAELVSLLEVYGRVQMRTRRLGHAKIYA 60

Qy 61 MHWATKLLMSASQCKLIWDSYTNTKVAIPRSSLWMCAYAPSGNEVACCGLDNM 120
Db 61 MHWGDYSRLLVSAASDQCKLIWDSYTNTKVAIPRSSLWMCAYAPSGNEVACCGLDNM 120

Qy 121 CSYNYLNKSREGNVKVSRELSAHTGYSCCRELDDNNIVSGDTCAALWDETGQKTVF 180
Db 121 CSYNYLNKSREGNVKVSRELSAHTGYSCCRELDDNNIVSGDTCAALWDETGQKTVF 180

Qy 181 VGHGDCMSLAVSPDNLNFISGACASAKLWDYREGTCQFTGHSNDINACIFPPNGEA 240
Db 181 TGHDGDMVMSLISPDLKFVSGACDASSKLWDYREGTCQFTGHSNDINAVSFPSGYA 240

Qy 241 ICGSDDASCRFLDLRAQELICFHESIIGITSTAFSLSGRLIPAGYDFNCNWDSM 300
Db 241 FANGDDATCRLFDRAQELICFHESIIGITSTAFSLSGRLIPAGYDFNCNWDSM 300

Qy 301 KSEFVGILSGLHDNRVNSCLGVTAQDGMAVATGSMDSEFLKIWN 340
Db 301 KGRRGVLAQHDKRNSCLGVTDGMAVATGSMDSEFLKIWN 340

RESULT 10

S3348 GTP-binding regulatory protein beta chain - great pond snail
N;Alternate names: guanine nucleotide regulatory protein beta chain
C;Species: Lymnaea stagnalis (great pond snail)
C;Accession: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S24348

R;Krol, J.C.; Novers, E.; van Kesteren, E.R.; Planta, R.J.; Vreugdenhil, E.; van Heerik
Biochim. Biophys. Acta 1222, 129-133, 1994
A;Title: A G-protein beta subunit that is expressed in the central nervous system of the
A;Reference number: S69891; MUID:94242793
A;Accession: A62617
A;Molecule type: mRNA
A;Residues: 1-326 <PON>
A;Cross-references: GB:M16480; NID:9163112; PIDN:AAA30553_1; PID:9163113
R;Gao, B.; Gilman, A.G.; Robishaw, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
A;Title: A second form of the beta subunit of signal-transducing G proteins.
A;Reference number: R94177; MUID:87317607
A;Accession: A82040
A;Molecule type: mRNA
A;Residues: 88-270; V, 272-302 <GAO>

C;Cross-references: GB:MG6539; NID:9163110; PIDN:AAA30552_1; PID:9163111
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rare; it is specific for each type of G protein.

C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C;Keywords: GTP binding; heterotrimer; signal transduction

F;37-70/Domain: WD repeat homology <WD1>

F;74-112/Domain: WD repeat homology <WD2>
F;125-157/Domain: WD repeat homology <WD3>
F;166-199/Domain: WD repeat homology <WD4>
F;208-241/Domain: WD repeat homology <WD5>
F;249-285/Domain: WD repeat homology <WD6>
F;294-326/Domain: WD repeat homology <WD7>

Query Match 81.2%; Score 1469; DB 1; Length 326;

Best Local Similarity 80.7%; Pred. No. 3.1e-16; Matches 263; Conservative 30; Mismatches 33; Indels 0; Gaps 0; C;Accession: F52-85/Domain: WD repeat homology <WD1>
F;181-214/Domain: WD repeat homology <WD2>
F;257-300/Domain: WD repeat homology <WD3>
F;309-341/Domain: WD repeat homology #status atypical <WD7>

Query Match 81.8%; Score 1480; DB 2; Length 341;

Best Local Similarity 79.6%; Pred. No. 3.9e-17; Matches 269; Conservative 30; Mismatches 39; Indels 0; Gaps 0; C;Accession: D4 DDEALRQETEQLKNQIREBARKAGDTTLAQASGVAVGRQMRTRRLGHAKIYAH 63
Db 63 WADSKLVLVSAASDGKLIWDSYTNTKVAIPRSSLWMCAYAPSGNFVACGLDNMC 122
Db 64 WASDRSLNLVSAASDGKLIWDSYTNTKVAIPRSSLWMCAYAPSGNFVACGLDNMC 123

Qy 123 YN1KSREGNVSKSRELSAHTSYLSCCREFLDDNNIVSGDTCAALWDETGQKVYFG 182
Db 124 YSLKTRREGNVRSRELPGHTGYSLLSCCRIDDNSIVTSQGMDCALWDETGQTSFTG 183

Qy 183 HTGDOMSLAVSPDENLFTSGACASAKLWDVRGCTRCOTFIGHESDINAICEFPNGEAIIC 242
Db 184 HTGDMVMSLTSRDPRTFVSGACDASAKLWDVRGCMKOTESHDINAITYFPNGHAF 243

Qy 243 TGSDDASCRFLDLRAQELICFHESIIGITSTAFSLSGRLIPAGYDFNCNWDSM 302
Db 244 TGSDDATCRLFDRAQELICFHESIIGITSTAFSKSGRLILGRYDDFNQNCNWVDLKQ 303

Qy 303 ERVGLSGHDNRVNSCLGVTAQDGMAVATGSMDSEFLKIWN 340
Db 304 ETGVLLAGHDNRVNSCLGVTEDGSAVATGSMDSEFLKIWN 341

RESULT 11

RGB02 GTP-binding regulatory protein beta-2 chain - bovine (fragment)
C;Alternname: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992
C;Accession: A26617; A28040

R;Fong, H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 84, 3792-3796, 1987
R;Gao, B.; Gilman, A.G.; Robishaw, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
A;Title: Distinct forms of the beta subunit of GTP-binding regulatory proteins identi
A;Reference number: A94155; MUID:87231903

A;Accession: A26617
A;Molecule type: mRNA
A;Residues: 1-326 <PON>
A;Cross-references: GB:M16480; NID:9163112; PIDN:AAA30553_1; PID:9163113

A;Title: A second form of the beta subunit of signal-transducing G proteins.
A;Reference number: R94177; MUID:87317607
A;Accession: A82040

A;Molecule type: mRNA
A;Residues: 88-270; V, 272-302 <GAO>

C;Cross-references: GB:MG6539; NID:9163110; PIDN:AAA30552_1; PID:9163111
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rare; it is specific for each type of G protein.

C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C;Keywords: GTP binding; heterotrimer; signal transduction

F;37-70/Domain: WD repeat homology <WD1>

F;74-112/Domain: WD repeat homology <WD2>
F;125-157/Domain: WD repeat homology <WD3>
F;166-199/Domain: WD repeat homology <WD4>
F;208-241/Domain: WD repeat homology <WD5>
F;249-285/Domain: WD repeat homology <WD6>
F;294-326/Domain: WD repeat homology <WD7>

Query Match 81.2%; Score 1469; DB 1; Length 326;

Best Local Similarity 80.7%; Pred. No. 3.1e-16; Matches 263; Conservative 30; Mismatches 33; Indels 0; Gaps 0; C;Accession: F52-85/Domain: WD repeat homology <WD1>
F;181-214/Domain: WD repeat homology <WD2>
F;257-300/Domain: WD repeat homology <WD3>
F;309-341/Domain: WD repeat homology #status atypical <WD7>

Qy 15 IKKQIADARKACADVTIAELVSLLEVYGRVQMRTRRLGHAKIYAHWDKLSLUVAS 74

Db 1 RNRQIRDARKACGDSTLQTQITAGLPVQRIQTRTRLGHAKIYAMHWGTDLSRILVAS 60
 Qy 75 QDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 134
 Db 61 QDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 120
 Qy 135 VSRLELSAHTGYLSCRETFDDNNIVTSSGDTCALMDIETGQOKTVFVG 194
 Db 121 VSRELPGHTGYLSCRCFLDDNNIVTSSGDTCALMDIETGQOKTVFVG 180
 Qy 195 DNLFTSGACDASAKLWDVDRSMCROTCRQFTGHESDINAICFPNGEACTSSDASCRLF 254
 Db 181 DGRTPFVSGACDASAKLWDVDRSMCROTCRQFTGHESDINAICFPNGEACTSSDASCRLF 240
 Qy 255 LRADQELICFSHESIICGITSVAFSISGRLLFAGYDFNCNWDSMSKSERVGIISGHDR 314
 Db 241 ERAGVLAGHDRVSCLGIVTEDGMAVATGSWDSFLKINN 300
 Qy 315 VSCLGIVIADGMAVATGSWDSFLKINN 340
 Db 301 VSCLGIVTDDGMAVATGSWDSFLKINN 326

RESULT 12
 RCOBEE
 GTP-binding regulatory protein beta chain - northern European squid
 N;Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C;Species: Loligo forbesi (northern European squid)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C;Accession: S13302
 R;Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Findlay, J.B.C.
 Biochem. J. 273, 225-228, 1991
 A;Title: Sequence of the beta-subunit of the phosphatidylinositol-specific phospholipase
 A;Reference number: S13302; MUID:91113146
 A;Accession: S13302
 A;Molecule type: mRNA
 A;Residues: 1-341 <YAR>
 A;Cross-references: GB:M22567; GB:J04083; NID:9157497; PIDN:AB59247.1; PID:9157498
 C;Genetics:
 A;Gene: FLYBase:Gbg
 A;Cross-references: FlyBase:FBgn0001105
 A;Map position: X13F
 C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F;51-84/Domain: WD repeat homology <WD1>
 F;88-126/Domain: WD repeat homology <WD2>
 F;180-213/Domain: WD repeat homology <WD4>
 F;222-255/Domain: WD repeat homology <WD5>
 F;283-299/Domain: WD repeat homology <WD6>
 F;308-340/Domain: WD repeat homology <WD7>

Query Match 80.7%; Score 1459; DB 1; Length 340;
 Best Local Similarity 77.4%; Pred. No. 2..3e-15; Gaps 42; Indels 0; Gaps 0;
 Matches 263; Conservative 35; Mismatches 42; Gaps 0;

Db 1 MGEMEQLRQEACOLKKQADARKACADVTALAEVLGVLEVGVRQMRTRLGHAKIYA 60
 Qy 61 MHWATDSLKLVSASQDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 120
 Db 61 MHWGNDSLNLVSAQDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 120
 Qy 121 CSYLNKRSREGKVRSBELSATGYLSCCRETFDDNNIVTSSGDTCALMDIETGQOKTVF 180
 Db 121 CSYLNKRSREGKVRSBELPGHGGYLSCCRFLDDNNIVTSSGDTCALMDIETGQOKTVF 180
 Qy 181 VGTGDOMSLAVSPDENLFIISACDASAKLWDVREGTCRQFTGHESDINAICFPNGE 240
 Db 181 LIGHGDYMAISLAPOCKTFVSGACDASAKLWDIREGVCKOPFGHESDINAIVTFFPNGA 240
 Qy 241 ICGSDDASCRFLDRAQELICFSHESIICGITSVAFSISGRLLFAGYDFNCNWDSM 300
 Db 241 FATGSDDATCRFLDIRADQELAMYSHDNITCGITSVAFSRSGRLLLAGYDDEENWDM 300
 Qy 301 KSERVGLSGHNRVSLGIVIADGMAVATGSWDSFLKINN 340
 Db 301 KAERSGLAGHDRVSCLGIVTEDGMAVATGSWDSFLKINN 340

RESULT 14
 M47370
 GTP-binding regulatory protein beta chain - slime mold (Dictyostelium discoideum)
 C;Species: Dictyostelium discoideum
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C;Accession: A47370
 R;Lilly, P.; Wu, L.; Weller, D. L.; Devreotes, P. N.
 Genes Dev. 7, 986-995, 1993

Db 244 TGSDDATCRFLDIRADQELAMYSHDNITCGITSVAFSRSGRLLLAGYDDEENWDM 303
 Qy 303 ERVGLISGHNRVSLGIVIADGMAVATGSWDSFLKINN 340
 Db 304 ERAGVLAGHDRVSCLGIVTEDGMAVATGSWDSFLKINN 341

RESULT 13
 RGFFBH
 GTP-binding regulatory protein beta chain homolog - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C;Accession: A40489
 R;Yarfitz, S.; Provost, N.M.; Hurley, J.B.; Proc. Natl. Acad. Sci. U.S.A. 85, 7134-7138, 1988
 A;Title: Cloning of a Drosophila melanogaster guanine nucleotide regulatory protein b
 A;Reference number: A40489; MUID:89017152
 A;Accession: A40489
 A;Molecule type: mRNA
 A;Residues: 1-340 <YAR>
 A;Cross-references: GB:M22567; GB:J04083; NID:9157497; PIDN:AB59247.1; PID:9157498
 C;Genetics:
 A;Gene: FLYBase:Gbg
 A;Cross-references: FlyBase:FBgn0001105
 A;Map position: X13F
 C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F;51-84/Domain: WD repeat homology <WD1>
 F;88-126/Domain: WD repeat homology <WD2>
 F;180-213/Domain: WD repeat homology <WD4>
 F;222-255/Domain: WD repeat homology <WD5>
 F;283-299/Domain: WD repeat homology <WD6>
 F;308-340/Domain: WD repeat homology <WD7>

Query Match 80.7%; Score 1459; DB 1; Length 340;
 Best Local Similarity 77.4%; Pred. No. 2..3e-15; Gaps 42; Indels 0; Gaps 0;
 Matches 263; Conservative 35; Mismatches 42; Gaps 0;

Db 1 MGEMEQLRQEACOLKKQADARKACADVTALAEVLGVLEVGVRQMRTRLGHAKIYA 60
 Qy 61 MHWATDSLKLVSASQDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 120
 Db 61 MHWGNDSLNLVSAQDGKLIWDSYTNTKVAIPRLRSSWVMTCAYAPSGNEVACGGIDNNCSIYNIKSREGNV 120
 Qy 121 CSYLNKRSREGKVRSBELSATGYLSCCRETFDDNNIVTSSGDTCALMDIETGQOKTVF 180
 Db 121 CSYLNKRSREGKVRSBELPGHGGYLSCCRFLDDNNIVTSSGDTCALMDIETGQOKTVF 180
 Qy 181 VGTGDOMSLAVSPDENLFIISACDASAKLWDIREGVCKOPFGHESDINAIVTFFPNGA 240
 Db 181 LIGHGDYMAISLAPOCKTFVSGACDASAKLWDIREGVCKOPFGHESDINAIVTFFPNGA 240
 Qy 241 ICGSDDASCRFLDRAQELICFSHESIICGITSVAFSISGRLLFAGYDFNCNWDSM 300
 Db 241 FATGSDDATCRFLDIRADQELAMYSHDNITCGITSVAFSRSGRLLLAGYDDEENWDM 300
 Qy 301 KSERVGLSGHNRVSLGIVIADGMAVATGSWDSFLKINN 340
 Db 301 KAERSGLAGHDRVSCLGIVTEDGMAVATGSWDSFLKINN 340

A; Title: A G-protein beta-subunit is essential for Dictyostelium development.
 A; Reference number: A47370; MUID:93279474
 A; Status: preliminary
 A; Residues: 1-347 <tilde>
 A; Cross-references: GB:373641; NID:9660980; PIDN:CA52018.1; PID:9460981
 C; Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F; 18-220/Domain: WD repeat homology <WD2>
 F; 273-306/Domain: WD repeat homology <WD3>
 F; 315-347/Domain: WD repeat homology #status atypical <WD6>

Query Match 68.4%; Score 1238; DB 2; Length 347;
 Best Local Similarity 66.7%; Preq. No. 9.6e-97; Mismatches 47; Indels 2; Gaps 1;
 Matches 226; Conservative 47; MisMatches 64;

Qy 3 EMEQLROEAQQLKQTADARKACADVLAELVLGSLEVGVRQV-MRTRRLRGHLAKIYA 60
 Db 8 KIQQARDAESKEQITRANRDVMDNTLTKTFTRDPLPGPKMEGKIKVRENLKHLAKIYA 67

Qy 61 MIWATPSKLIVSASODGKLIWDSYTINKHAILRSSLSSWMTCAVAPSGNFVAGGLDN 120
 Db 68 MHWAEWDVHLVYASQDGKLIWDSYTINKHAILRSSLSSWMTCAVAPSGNFVAGGLDN 120

Qy 121 CSYLNLSKRSREGNVKVSRELSAHTSYLISCCRFLDDNNIVSSGDTCAWLDEGGQKUVE 180
 Db 128 CSYLNLSKRSREGPVRCRELNSHTGYLSCCRFLNDRQIVTSSGDMTCILWDENGTKTEF 187

Qy 181 VGHGDCCMSLAVSPFLNLETSQAGDASAKLWDYREGTGTQRTFGHESDINAICFFNEA 240
 Db 188 SDHNGDVMVSVPDKNYFISGADATAKLWDISRGKCVQFTGHEADINAVOYFPNGLS 247

Qy 241 ICTSSDDASCRLEFLRADOLELICFSHESITCGITSVAFSLSGRLPLAGYDFNCNWDSM 300
 Db 248 FGTTSSDDASCRLEFLRADOLELICFSHESITCGITSVAFSLSGRLPLAGYDFNCNWDSM 307

Qy 301 KSERVGLLSGHDNWKVSCIGVTADGMAYATGSMSDFLKIW 339
 Db 308 KGERVLSLTGHNRYVSCIGVPTDGMALCTGSMSDLSLKIW 346

RESULT 15

A54969
 beta-5 GTP-binding protein - mouse
 C; Species: Mus musculus
 C; Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Aug-1999
 R; Accession: A54969
 R; Watson, A.J.; Katz, A.; Simon, M.I.
 J. Biol. Chem. 269, 22150-22156, 1994
 A; Title: A fifth member of the mammalian G-protein beta-subunit family. Expression in brain
 A; Reference number: A54969; MUID:94350964
 A; Accession: A54969
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-353 <WAT>
 A; Cross-references: GB:L14290; NID:91237255; PIDN:AA93084.1; PID:9557738
 C; Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F; 59-226/Domain: WD repeat homology <WD1>
 F; 149-182/Domain: WD repeat homology <WD3>
 F; 193-226/Domain: WD repeat homology <WD4>
 F; 270-312/Domain: WD repeat homology <WD5>
 F; 321-353/Domain: WD repeat homology #status atypical <WD7>

Query Match 52.4%; Score 948.5; DB 2; Length 353;
 Best Local Similarity 51.9%; Preq. No. 2.4e-72; Mismatches 57; Indels 5; Gaps 3;

Matches 177; Conservative 57; MisMatches 102; Indels 5; Gaps 3;

Qy 4 MEQRRQEABQLKIQIADARKACADVLAELVSGLEVGVRQVOMRTRRLGHLAKIYAMHW 63
 : | : ||| | :: | | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 12 LASLKSEAESSLKGKLEERAKLHDVELHQVAERVEALGQFWKTRTRLKGHGKVKLCMDW 71
 Qy 64 ATDSKLVNEASQDGKLIWDSYTINKHAILRSSLSSWMTCAVAPSGCATAGGGLDDNMCST 123
 Db 72 CKDRRTVSSQDGKVIWDSYTINKHAILRSSLSSWMTCAVAPSGCATAGGGLDDNMCST 131
 Qy 124 YNL--KSRBGGNVKVSRELSAHTSYLISCCRFLDDNNIVSSGDTCAWLDEGGQKUVE 180
 Db 132 YPLFDKNNEMAKKSVAMHINYLSCACSFNSDMOILTGSGDGTACALNDESCQLOSF 191
 Qy 181 VGHGD--CMLSLAVSPFLNLETSQAGDASAKLWDYREGTGTQRTFGHESDINAICFFNG 238
 Db 192 HGHCADVCLDLAPSETGNTVSGGCDKAKMWDRSGQCVOAETHEDVNSVRYIPG 251
 Qy 239 EAICTGSDASCRLEFLRADOLELICFSHESITCGITSVAFSLSGRLPLAGYDFNCNWDSM 298
 Db 252 DAFASSDDAATCRLYDRADEVAISYKLSLGRASSDSDPFSGRLLFAGYDNYTINWD 339
 Db 312 VLKGSRVSIIFGHENRVSILRSPDGTARFCGSMDHTLRW 352

Search completed: September 28, 2001, 10:33:21
 Job time: 272 sec

Fri Sep 28 10:45:14 2001

us-09-492-029-5.rpr

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:34:28 ; search time 16.71 Seconds
 (without alignments)
 697.000 Million cell updates/sec

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEMEGIQLRQEAEQLKQIAD..... TADGNAVATGSWDSLKIWN 340

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1809	100.0	340	1 GBB3_HUMAN	PI16520 homo sapien
2	1763	97.5	340	1 GBB3_MOUSE	Q61011 mus musculus
3	1762	97.5	340	1 GBB3_RAT	PS2287 rattus norvegicus
4	1759	97.2	340	1 GBB3_CANFA	PF79147 canis familiaris
5	1578	87.2	340	1 GBB1_HUMAN	PO4301 homo sapiens
6	1573	87.0	340	1 GBB1_XENLA	PT79559 xenopus laevis
7	1572	86.9	340	1 GBB1_RAT	PF54311 rattus norvegicus
8	1528	84.5	340	1 GBB2_HUMAN	PF1016 hominidae
9	1521	84.1	340	1 GBB2_MOUSE	PT54312 mus musculus
10	1520	84.0	340	1 GBB1_GREEEL	PF1743 caenorhabditis elegans
11	1500	82.9	340	1 GBB2_RAT	PT54313 rattus norvegicus
12	1500	82.9	340	1 GBB4_MOUSE	PT29387 mus musculus
13	1480	81.8	341	1 GBB1_LINST	Q08706 linum usitatissimum
14	1479	81.8	340	1 GBB1_HOMAM	Q45040 homarus americanus
15	1469	81.2	326	1 GBB2_BOVIN	PT1017 bos taurus
16	1463	80.9	341	1 GBB1_LOFO	PT2332 loligo forbesi
17	1459	80.7	340	1 GBB1_DRONE	PT26308 drosophila melanogaster
18	1459	80.7	340	1 GBB1_DICDI	PT36408 dictyostelia intestinalis
19	1198	66.2	359	1 GBB1_CRYPA	Q14435 cryptophene crassa
20	949.5	52.5	353	1 GBB5_HUMAN	Q14775 homo sapiens
21	948.5	52.4	353	1 GBB5_MOUSE	PT54314 mus musculus
22	927.5	51.3	356	1 GBB5_GAEL	Q26036 caenorhabditis elegans
23	847	46.8	380	1 GBB1_ORRSA	Q40587 oryza sativa
24	831	45.7	380	1 GBB1_MAZE	PT49178 zeaxanthin
25	824	45.6	377	1 GBB1_TOBAC	PF53397 nicotiana tabacum
26	822	45.4	375	1 GBB3_TOBAC	Q40507 nicotiana tabacum
27	822	45.3	377	1 GBB2_TOBAC	PT93398 nicotiana tabacum
28	822	45.4	377	1 GBB1_SOLTU	PT93563 solanum tuberosum
29	815	45.1	377	1 GBB1_ARITH	PA49157 arabidopsis thaliana
30	808	45.7	346	1 GBB2_DRONE	PT29329 drosophila melanogaster
31	790	43.7	377	1 GBB2_NICPL	PF53339 nicotiana plumbaginifolia
32	668	36.9	375	1 GBB1_SCIPRO	Q103082 schizosaccharomyces pombe
33	647	35.8	403	1 GBB1_YEAST	PT93512 saccharomyces cerevisiae

ALIGNMENTS

Query Match 100 %; Score 1809; DB 1; Length 340;
Best Local Similarity 100 %; Pred. No. 1.5e-152; Mismatches 0; Indels 0; Gaps 0;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60
Db 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60

Qy 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120
Db 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120

Qy 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180
Db 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180

Qy 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240
Db 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240

Qy 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300
Db 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300

RESULT 2

GBB3_MOUSE STANDARD PRT: 340 AA.

ID GBB3_MOUSE STANDAR; PRT: 340 AA.

AC 061011; (Rel. 35, Created) 15-JUL-1998 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)

DE QUANTINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3 DE (TRANSDUCIN BETA CHAIN 3). GN GNB3.

OS Mus musculus (Mouse) OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Butheria: Rodentia: Sciurognathi: Muridae: Murinae; MUS. NCBI_TaxId=1090; [1]

RP SEQUENCE FROM N.A. Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,

RJ Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W., Gibbs R.A.; Submitted (ANG-1997) to the EMBL/GenBank/DDBJ databases. RN [2] SEQUENCE OF 199-301 FROM N.A. RP STRAIN=CF-1 / HARIAN; TISSUE=Retina; RC RX MEDLINE-97011591; PubMed=858601; RA Williams C.J., Schultz R.M., Kopf G.S.; RT "G protein gene expression during mouse oocyte growth and maturation, and preimplantation embryo development."; RL Mol. Reprod. Dev. 44:315-323(1996).

DR PRINTS; PRO0320; GPROTEINBRP.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS5082; WD_REPEATS_2; 5.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR PRINTS; PRO0319; GPROTEINB.
FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
SQ SEQUENCE 340 AA; 37221 MW: 896706461B8074F CRC64;

Query Match 97.5%; Score 1763; DB 1; Length 340;
Best Local Similarity 97.1%; Pred. No. 1.7e-148; Mismatches 5; Indels 5; Gaps 0;
Matches 330; Conservative 5; Mismatches 5; Indels 5; Gaps 0;

Qy 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60
Db 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60

Qy 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120
Db 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120

Qy 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180
Db 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180

Qy 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240
Db 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240

Qy 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300
Db 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300

Query Match 97.5%; Score 1763; DB 1; Length 340;
Best Local Similarity 97.1%; Pred. No. 1.7e-148; Mismatches 5; Indels 5; Gaps 0;
Matches 330; Conservative 5; Mismatches 5; Indels 5; Gaps 0;

Qy 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60
Db 1 MGEMEQLRQEAEQLKKQIADARKAKACADVIAELAELSGLEVGVRVOMRTTRTGLHLAKYA 60

Qy 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120
Db 61 MHWATDSKLIVSASODGKLTIVWDSDSYTTNKVHAIPRPLRSWNMTCAVAPSGNFWACGGIDNM 120

Qy 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180
Db 121 CSYNLKSREGNYKVSRLESAHTGVLSCCFLDDNNITVSSGDTCALWDIETGQKTVF 180

Qy 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240
Db 181 VGHGDCLMSLAVSPPNLFISGACDASKLMDVREGTCRFTGHESDINAICFFPNEA 240

Qy 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300
Db 241 ICTGSDASCRFLDRADEOELICFSHESIICGITSVAFLSGRLIFAGYDDFNCVWDSM 300

FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37144 NW: 8E3B5A528E29C37 CRC64;

Query Match 97.2%; Score 1759; DB 1; Length 340;
 Best Local Similarity 96.8%; Pred. No. 3; ge=48;
 Matches 329; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 SPECIES=Bovine;
 RC MEDLINE=88030675; PubMed=2414128;
 RX Sugimoto K., Nukada T., Tanabe T., Takahashi H., Noda M., Minamino N.,
 RA Kawaga K., Matsuo H., Hirose T., Inayama S., Numa S.;
 RT "Primary structure of the beta-subunit of bovine transducin deduced
 from the cDNA sequence";
 RT FEBS Lett. 191:235-240(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C familiaris;
 RX MEDLINE=97445667; PubMed=9300552;
 RA Kyima T., Paulin L., Hurwitz M.Y., Hurwitz R.L., Komonen B.;
 RT Cloning of the cDNA encoding rod photoreceptor
 degenerate Labrador retriever dog";
 RL Res. Vet. Sci. 62:293-296(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROPRIMER.
 BX MEDLINE=96107343; PubMed=8215505;
 RA Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
 RA Gilman A.G., Sprang S.R.;
 RT "The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma
 2." Cell 83:1047-1058(1995).
 RL RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.
 RX MEDLINE=96149354; PubMed=8552196;
 RA Sondek J., Bohm A., Lambright D.G., Hamm H.E., Sigler P.B.;
 RT "Crystal structure of a G-protein beta gamma dimer at 2.1-A
 resolution." Cell 37:369-374(1996).
 RL RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.
 RX MEDLINE=98416696; PubMed=9739091;
 RA Loew A., Ho Y.K., Blundell T., Box B.;
 RT "Phosducin induces a structural change in transducin beta gamma.";
 RL Structure 6:1007-1019(1998).
 CC -1- FUNCTION: GUAINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTASE ACTIVITY. FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC ---
 DR EMBL: X04526; CAA8207; 1;
 DR EMBL: U22055; AAC22905; 1;
 DR EMBL: X03073; CAA26875; 1;-
 DR EMBL: M13236; AAA0792; 1;-
 DR EMBL: M0540; AAC63265; 1;-
 DR EMBL: Z15134; CAA59446; 1;-
 DR PIR: A24853; RGHUB1;
 DR PIR: A24225; RGB01;
 DR PDB: 1GG2; 12-FEB-97.
 DR PDB: 1GP2; 12-FEB-97.
 DR PDB: 1TBG; 01-APR-97.
 DR PDB: 1AQI; 16-FEB-99.
 DR PDB: 1BXK; 23-FEB-99.
 DR PDB: 1BY7; 23-FEB-99.
 MIM: 139380; -.

RESULT 5
 GBL_HUMAN STANDARD; PRT: 340 AA.
 AC P04901; P04697;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TRANSDUCIN NUCLEOTIDE-BINDING PROTEIN G(I),G(S),G(T) BETA SUBUNIT 1
 DR (TRANSDUCIN BETA CHAIN 1).
 GS GNB1.
 GO Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606, 10090, 9913, 9615;
 RN 111
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Liver;
 RX MEDLINE=87030912; PubMed=309547;
 RA Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;
 RT "Beta-subunits of the human liver Gs/Gi signal-transducing proteins
 and those of bovine retinal rod cell transducin are identical.";
 RL FEBS Lett. 207:187-192(1986).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; TISSUE=Adrenal gland;
 RA Oiu R., Schimmer B.P.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine;
 RX MEDLINE=86177563; PubMed=3083416;
 RA Fong H.-K.W., Hurley J.B., Hopkins R.S., Maake-Lye R., Johnson M.S.,
 RA Doolittle R.F., Simon M.I.;

DR MGD: MGI: 95781; Grnl.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 PROSITE; PS00578; WD_REPEATS_1; 3.
 PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT REPEAT 71 71 V->L (IN REF. 4).
 SEQUENCE 340 AA; 37377 MW; 896CBD32D2686598 CRC64;

Query Match 87.2%; Score 1578; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 3.8e-12; Mismatches 25; Indels 0; Gaps 0;
 Matches 283; Conservative 32; MisMatches 25; Drs 0; Gaps 0;

QY 1 MGEMEQLQRQEAEOLKKQIADARKACADVTLAELVSGLEVNVRGVQMRTRTLLRHLAKIYA 60
 | :|:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 | :|:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 1 MSELDLQRQEASQDLKNIORDARKACADATLSQITNNDPVGRIQMTRTLLRHLAKIYA 60

QY 61 MHWATDSKLVLVASQDSKLIVWDSDYTNTNKVHAIPLLPSLSSWMTCAYAPSGNIVACGGIDNM 120
 |||:|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 |||:|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 61 MHWATDSKLVLVASQDSKLIVWDSDYTNTNKVHAIPLLPSLSSWMTCAYAPSGNIVACGGIDNM 120

QY 121 CSYNLKSREGNVKVSRELSAHTGYLSCREDDNNIVTSSGDTICALWDIETGQQKTVF 180
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 121 CSYNLKSREGNVKVSRELTAHTGYLSCREDDNNIVTSSGDTICALWDIETGQQKTVF 180

Db 181 VGHGDCMSLAVSPDPDNIFISGACDASAKLWDVREGTCRQFTGHSDINAICFFNGEA 240
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 181 TGHGDMVSLSLAPDTRFLVSGACDASAKLWDVREGMCQFTGHSDINAICFFNGNA 240

QY 241 ICTGSDDAASCRFLDLRADQELCFSHESITCGITSVAFSLSGRLLAGYDFFNCNWDSM 300
 |||:|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:
 |||:|||:|||||:|||:|||:|||:|||:|||:|||:
 241 FATGSDDATCRFLDLRADQELCFSHESITCGITSVAFSLSGRLLAGYDFFNCNWDSM 300

Qy 301 KSERVIGLISGHNRVSCLGVTADGMAVATGSWSDFLKWN 340
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 301 KADRAGVLAGHNRVSCLGVTADGMAVATGSWSDFLKWN 340

RESULT 6
 GBB1_XENLA STANDARD; PRT; 340 AA.
 ID GBB1_XENLA
 AC P79595;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1) (XGBEFA1).
 GN GNB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
 OC Xenopodinae; Xenopus.
 RN NCBI_TAXID=8355;
 [1] SEQUENCE FROM N.A.
 RX MEDLINE:97109512; Pubmed=8951792;
 RA Devic E., Paquereau L., Rizzoli K., Monier A., Knibehler B.,
 RA Audiger Y.;
 RT "The mRNA encoding a beta subunit of heterotrimeric GTP-binding
 proteins is localized to the animal pole of *Xenopus laevis* oocyte and
 embryos.";

RU Mech. Dev. 59:141-151 (1996).
 CC FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 -!- INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@lsb-sib.ch).
 CC
 DR EMBL: X86369; CAA60532; 1; -.
 DR HSSP: P04901; 1TBG.
 DR InterPro; IPR001632; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00578; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37330 MW; DEE36FER60A2D6A9 CRC64;

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 82.9%; Pred. No. 1.1e-131; Mismatches 27; Indels 0; Gaps 0;
 Matches 282; Conservative 31; MisMatches 27; Drs 0; Gaps 0;

QY 1 MGEMEQLQRQEAEOLKKQIADARKACADVTLAELVSGLEVNVRGVQMRTRTLLRHLAKIYA 60
 | :|:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 | :|:|||||:|||:|||:|||:|||:|||:|||:|||:
 1 MSELDLQRQEASQDLKNIORDARKACADATLSQITNNDPVGRIQMTRTLLRHLAKIYA 60

QY 61 MHWATDSKLVLVASQDSKLIVWDSDYTNTNKVHAIPLLPSLSSWMTCAYAPSGNIVACGGIDNM 120
 |||:|||:|||||:|||:|||:|||:|||:|||:|||:
 |||:|||:|||||:|||:|||:|||:|||:|||:
 61 MHWATDSKLVLVASQDSKLIVWDSDYTNTNKVHAIPLLPSLSSWMTCAYAPSGNIVACGGIDNM 120

QY 121 CSYNLKSREGNVKVSRELSAHTGYLSCREDDNNIVTSSGDTICALWDIETGQQKTVF 180
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 |||:|||:|||:|||:|||:|||:|||:|||:
 121 CSYNLKSREGNVKVSRELTAHTGYLSCREDDNNIVTSSGDTICALWDIETGQQKTVF 180

Db 181 VGHGDCMSLAVSPDPDNIFISGACDASAKLWDVREGTCRQFTGHSDINAICFFNGEA 240
 |||:|||:|||:|||:|||:|||:|||:|||:|||:
 181 TGHGDMVSLSLAPDTRFLVSGACDASAKLWDVREGMCQFTGHSDINAICFFNGNA 240

QY 241 ICTGSDDAASCRFLDLRADQELCFSHESITCGITSVAFSLSGRLLAGYDFFNCNWDSM 300
 |||:|||:|||||:|||:|||:|||:|||:|||:
 |||:|||:|||||:|||:|||:|||:|||:
 241 FATGSDDATCRFLDLRADQELCFSHESITCGITSVAFSLSGRLLAGYDFFNCNWDSM 300

Qy 301 KSERVIGLISGHNRVSCLGVTADGMAVATGSWSDFLKWN 340
 |||:|||:|||:|||:|||:|||:|||:|||:
 301 KADRAGVLAGHNRVSCLGVTADGMAVATGSWSDFLKWN 340

RESULT 7
 GBB1_RAT STANDARD; PRT; 340 AA.
 ID GBB1_RAT
 AC P54311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

Db	61	MHWASDRNLYSASQDGKLUWMDSTTNNKHATPLRSSWWTCAYAARGSYACGGDN	120
QY	121	CSIYNLKSRECVNVYSRELSAHTGYLSCCFLDDNTVSSGDPITCALWDIENGQKTVF	180
	: : : : : : : : : : : : :	: : : : : : : : : : : : :	
Db	121	CSISLXKTRREGNRVRSRELPHGTGILSCCRFLDDNQITTSGDMDTCAWLWIDETGOQTA	180
QY	181	VGHGCMMSLAVSPPPNLFGSGADASAKLWDVREGTORQTGFCHESDINAATCFPPNGEA	240
	: : : : : : : : : : : : :	: : : : : : : : : : : : :	
Db	181	TGHTGDMVSLSLSPDPRFTGACDASAKLWDVREGTORQTGFCHESDINAATCFPPNGEA	240
QY	241	ICTGSDASCLFLDRAQDQJLICFSHESTIGTISVAWSLSSRLFLAGVDFFCNWDSM	300
	: : : : : : : : : : : : :	: : : : : : : : : : : : :	
Db	241	FATGSDATCFLDIFDRAQDQELAMSHDNICIGTISVAWSKGRLLFAGYDFDRCNWDSDM	300
QY	301	KSERVGILSHDNRVSYCLGTYADGNAVATGSWDSFLKTNW	340
	: : : : : : : : : : : : :	: : : : : : : : : : : : :	
Db	301	QERAGVLAQHNDRVSYCLGVTDGMAVCTGSWDSFLKTNW	340
	: : : : : : : : : : : : :	: : : : : : : : : : : : :	
RESULT	11		
GBB2_RAT		STANDARD;	PRT;
ID			340 AA.
AC		P54313;	
RC		01-OCT-1996 (Rel. 34, Created)	
DT		01-OCT-1996 (Rel. 34, Last sequence update)	
DE		01-OCT-2000 (Rel. 40, Last annotation update)	
DE		GUANINE NUCLEOTIDE-BINDING PROTEIN G(I/G(S)/G(T) BETA SUBUNIT 2 (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).	
GN		GNB2.	
OS		Rattus norvegicus (rat).	
OC		Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX		NCBI_TAXID=10116;	
RN	[1]		
RP		SEQUENCE FROM N A.	
RA		STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;	
RC		Kuroda S., Tokunaga C., Konishi H., Kirkawa U.;	
RL		Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.	
CC		- - FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GPROTASE ACTIVITY. FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.	
CC		- - SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).	
CC		- - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).	
CC			
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC			
CC			
DR		EMBL: U34959; AAC72248.1; -.	
DR		HSSP: P04901; ITBG.	
DR		InterPro: IPR011632; -.	
DR		InterPro: IPR011680; -.	
DR		Pfam: PF00400; WD40; 7.	
DR		PRINTS: PR00319; GPROTEINB.	
DR		PRINTS: PR00320; GPROTEINB_RPT.	
DR		PROSITE: PS00678; WD_REPEATS_1; 3.	
DR		PROSITE: PS50022; WD_REPEATS_2; 6.	
DR		PROSITE: PS5024; WD_REPEATS_REGION; 1.	
KW		Transducer; Repeat; WD repeat; Multigene family.	
FT		REPEAT 53 83 WD 1.	
FT		REPEAT 95 125 WD 2.	
FT		REPEAT 141 170 WD 3.	
FT		REPEAT 182 212 WD 4.	
FT		REPEAT 224 254 WD 5.	
FT		REPEAT 268 298 WD 6.	
FT		REPEAT 310 340 WD 7.	
SQ		SEQUENCE 340 AA; 37500 MW; IAE60E2755C5B71BB CRC64;	

Query Match 82.9%; score 1500; DB 1; Length 340;
 Best Local Similarity 79.4%; Pred. No. 3e-125; Mismatches 270; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

DR MGD; MGT:104581; Gnb4.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00082; WD_REPEATS_2; 6.
 DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37354 MW; B21EEB29BA862B1E CRC64;

RESULT 12

GBB4_MOUSE STANDARD PRT; 340 AA.

AC P29387; 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CHAIN 4).

DB 301 KSERVGLISLGHDRNVRSLGVTDDGMAVATGSWDSFLKIWN 340

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Nematalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2181467; PubMed=1543505;

RA von Weizsaecker E., Strathmann M.P., Simon M.I.;
 RT "diversity among the beta subunits of heterotrimeric GTP-binding
 proteins: characterization of a novel beta-subunit CDNA.";
 RL Biochem. Biophys. Res. Commun. 183:350-356(1992),
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to licensed@isb-sib.ch).

CC

Query Match 82.9%; score 1500; DB 1; Length 340;
 Best Local Similarity 79.4%; Pred. No. 3e-125; Mismatches 270; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

DR MGD; MGT:104581; Gnb4.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00082; WD_REPEATS_2; 6.
 DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37354 MW; B21EEB29BA862B1E CRC64;

Query Match 82.9%; score 1500; DB 1; Length 340;
 Best Local Similarity 78.8%; Pred. No. 3e-125; Mismatches 34; Indels 0; Gaps 0;

Matches 268; Conservative 38; Mismatches 34;

DR 1 MGEMLQRLRQEQLKQIADARKACDVLAELVSGLEVGRVQMRTRFLRGHLAKIYA 60

DB 1 MSELQRLRQEQLNODIADARKACDVLAELVSGLEVGRVQMRTRFLRGHLAKIYA 60

DR 1 MSELQRLRQEQLNODIADARKACDVLAELVSGLEVGRVQMRTRFLRGHLAKIYA 60

DB 301 KSERVGLISLGHDRNVRSLGVTDDGMAVATGSWDSFLKIWN 340

OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 RX NCBI_TAXID=6523;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-CNS:

RX MEDLINE=94242793; PubMed=7514444;
 RA Knol J.C., Roovers E., van Kesteren E.R., Plantae R.J.,
 RA Vreugdenhil R., van Heerthuizen H.;
 RT "A G-protein beta subunit that is expressed in the central nervous
 system of the mollusc Lymnaea stagnalis identified through cDNA
 cloning.";
 RL Biochem. Biophys. Acta 1222:129-133(1994).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE

CC SIGNALING SYSTEMS - THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC DR RNL RN
DR RP RP
DR RX RX
DR RA RA
DR Xu F., Hollins B., Landers T.M., McClintock T.S.;
DR "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in
DR olfactory receptor neuron dendrites and brain neuropil."
DR RT J. Neurobiol. 36:525-536(1998).
DR PROSITE: PS00319; GPROTEINB.
DR PRINTS: PR00320; GPROTEINBPT.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS0082; WD_REPEATS_2; 5.
DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
DR KW Transducer; Repeat; WD repeat.
FT REPEAT 54 84 WD 1.
FT REPEAT 96 126 WD 2.
FT REPEAT 142 171 WD 3.
FT REPEAT 183 213 WD 4.
FT REPEAT 225 255 WD 5.
FT REPEAT 269 299 WD 6.
FT REPEAT 311 341 WD 7.
FT SEQUENCE 341 AA; 37320 MW; 4A266258387592E CRC64;

Query Match 81.8%; Score 1480; DB 1; Length 341;
Best Local Similarity 79.6%; Pred. No. 1.e-123;
Matches 269; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMEQLRQEAEQIKKQDADAKACDVTLAELVSGLEVNRYQMRRTLGLHLAKIYAMH 62
Db 4 DIELARLOTEEQIKKQDADAKACDVTLAELVSGLEVNRYQMRRTLGLHLAKIYAMH 63

Qy 63 WATDKSKLLVASQDGKLIVWDSYTNTKVAHPLRSSWVMTCAVAYSGNFVACGGLDNCS 122
Db 64 WASDSRNLVVASQDGKLIVWDSYTNTKVAHPLRSSWVMTCAVAYSGNFVACGGLDNCS 123

Qy 123 INLKLSREGNVKVSRELSAHTGCGYLSCRCFLDDNNTVTSSGDTCAWLIDETGQQTIVFGV 182
Db 124 IYSLKIREGVNVRSRELPGHGYLSCRCFLDDNNTVTSSGMSCLAWDINGQQTISFTG 183

Qy 183 HPGDCMMLAVSPDPFLNLITSGACDASAKLWDYREGTCRQTFGHESDINAATCFFPGEAIC 242

Db 184 HPGDVMSLSTSPDFRTVSGACDASAKLWDYRGCKQKQTSQHESDINAATYFPNGHAFIA 243

Qy 243 TGSDDASCRLEDRLRADOLELICHSHESTIGITSVAFSLSGRLFAGYDDNCVNDMSK 302
Db 244 TGSDDATCRLFDIRADOEIGMYSHDNITCIGITSVAFSKSGRLLGRRYDDNCVNDLQK 303

Qy 303 ERVGILSGHDNRIVSCLGWTAGDMVAVATGSMWSFLKIWN 340
Db 304 ETHGVLAGHDNRIVSCLGWTEDGSAVATGSMWSFLKIWN 341

RESULT 14
GB1L_HOMM
ID GB1L_HOMM
AC 045040;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GURANINE NUCLEOTIDE-BINDING PROTEIN G(I)(G(S)(G(T)) BETA SUBUNIT 1
DE (TRANSPORTIN BETA CHAIN 1).

GN Gbeta1.
OS Homarus americanus (American lobster).
OC Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Plocoyemata; Astacida;
OC Nephozoidea; Nephrlopidae; Homarus.
OC NCBI_TaxID=6706;
OX {1}
RN SEQUENCE FROM N.A.
RP MEDLINE=98410740; PubMed=9740024;
RX
RA
RT
RT
RT
RT
J. Neurobiol. 36:525-536(1998).
CC -!- FUNCTION: GUANINE NUCLEOTIDE BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC DR EMBL: AF044735; AAC02998 1; -.
DR InterPro: IPRO01632; -.
DR InterPro: IPRO01680; -.
DR Pfam: PF00400; WD40; -.
DR PRINTS: PR00319; GPROTEINB.
DR PROSITE: PR00320; GPROTEINBPT.
DR PROSITE: PS00319; GPROTEINB.
DR PROSITE: PS00678; WD_REPEATS_1; 3.
DR PROSITE: PS0082; WD_REPEATS_2; 6.
DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
DR KW Transducer; Repeat; WD repeat; Multigene family.
FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
FT SEQUENCE 340 AA; 37409 MW; 3483245F9291D82E CRC64;

Query Match 81.8%; Score 1479; DB 1; Length 340;
Best Local Similarity 78.2%; Pred. No. 2.1e-123;
Matches 266; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAEQIKKQDADAKACDVTLAELVSGLEVNRYQMRRTLGLHLAKIYA 60
Db 1 MNLDLSLRQEAEQIKKQDADAKACDVTLAELVSGLEVNRYQMRRTLGLHLAKIYA 60

Qy 61 MHWARDSKLLVASQDGKLIVWDSYTNTKVAHPLRSSWVMTCAVAYSGNFVACGGDNM 120
Db 61 MHWGDSRNLVVASQDGKLIVWDSYTNTKVAHPLRSSWVMTCAVAYSGNFVACGGDNM 120

Qy 121 CSIYNLKSREGNVKVSRELSAHTGCGYLSCRCFLDDNNTVTSSGDTCAWLIDETGQQTIVFGA 240
Db 181 TGHGDCMMLAVSPDPFLNLITSGACDASAKLWDYREGTCRQTFGHESDINAATCFFPGEA 240
Db 121 CSISLKLTRBGNVRVRSRELPGHGYLSCRCFLDDNNTVTSSGDTCAWLIDETGQQTIVFGA 240
Qy 181 VGHGDCMMLAVSPDPFLNLITSGACDASAKLWDYREGTCRQTFGHESDINAATCFFPGEA 240
Db 181 TGHGDCMMLAVSPDPFLNLITSGACDASAKLWDYREGTCRQTFGHESDINAATCFFPGEA 240
Db 241 ICTGSDASCRLEDRLRADOLELICHSHESTIGITSVAFSLSGRLFAGYDDNCVNDMS 300
Qy 241 ICTGSDASCRLEDRLRADOLELICHSHESTIGITSVAFSLSGRLFAGYDDNCVNDMS 300
Db 241 FATGSDATCRLFDIRADOEIGMYSHDNITCIGITSVAFSKSGKLLAGYDDNCVNDMS 300

Fri Sep 28 10:45:15 2001

QY 301 KSEERVGILSGHONRVSGLGVADGMATGSMDSFLKIWN 340
 Db 301 RTERAVGLAGHDNRVSCLGVIEDGMATGSMDSFLKIWN 340

RESULT 15
 GBB2_BOVIN STANDARD; PRT; 326 AA.
 AC P1017;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-90 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
 GN (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Bovinae; Bovidae; Bos.
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H. K. W., Amatruda T.T., IIT, Birren B.W., Simon M.I.;
 RT Proteins identified by molecular cloning ";
 RT proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 RN [2]
 RP SEQUENCE OF 88-302 FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 RT "A second form of the beta subunit of signal-transducing G proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 -I- IDENTIFIED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 -I- SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 -I- GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 -I- EFFECTOR INTERACTION.

-I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ispb-sib.ch/announce/> or send an email to license@ispb-sib.ch).

DR EMBL: M16480; AAA30553.1; --.
 DR EMBL: M16431; AAA62717.1; --.
 DR EMBL: M16539; AAA30552.1; --.
 DR PIR: A26617; RGBOB2.
 DR HSSP: P04901; IGP2.
 DR InterPro: IPR01680; --.
 DR Pfam: PF00440; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW transducer; Repeat; WD repeat; Multigene family.
 FT NON_TER 1
 FT REPEAT 39 WD 1.
 FT REPEAT 81 WD 2.
 FT REPEAT 127 WD 3.
 FT REPEAT 168 WD 4.
 FT REPEAT 210 WD 5.
 FT REPEAT 254 WD 6.
 FT REPEAT 296 WD 7.
 FT REPEAT 326 AA; L->V (IN REF. 2).
 SQ SEQUENCE 326 AA; 35645 MW; EEB90EF5BC51B23 CRC64;

Search completed: September 28, 2001, 10:34:29
 Job time: 284 sec

	Best Local Similarity	Pred	No.	Indels	Gaps
Matches	80.7%	No.	1.6e-122	0	0;
Db	1 RNQIRDARKACGDSLTLQTAGLDPVGRITMRTRTLGHAKTYAMHWGTDLSRLVSA	QY	15 KQQTADARKACADVLAELVSLGVWGRQMRRTLGHAKTYAMHWGTDLSRLVSA	74	60
Db	1 QDGKLUITWDSYTNNKVHAIPLRSWWMCAVAPSGNFVACGGLDNMSIYNIKSREGNK	QY	75 QDGKLUITWDSYTNNKVHAIPLRSWWMCAVAPSGNFVACGGLDNMSIYNIKSREGNK	134	120
Db	121 VSRELSSAHGILSCLRFDDNNTVSSDPTALWDETGQRTVFGHTGQMSLAVP	QY	135 VSRELSSAHGILSCLRFDDNNTVSSDPTALWDETGQRTVFGHTGQMSLAVP	194	180
Db	181 DGRPFVSGACDASKLWDREGCROTFGHEDINAICFFNGEAICTGSDDASERLF	QY	195 DNLIFLISGACDASKLWDREGCROTFGHEDINAICFFNGEAICTGSDDASERLF	254	240
Db	255 LRAQDELLCFSHHSIICTTSVAFSLSGRLLAGYDFNCNWDSKSERVGLSGHNR	QY	255 LRAQDELLCFSHHSIICTTSVAFSLSGRLLAGYDFNCNWDSKSERVGLSGHNR	314	300
Db	241 LRAQDELLIMIYSHDNIICGITSYAFSRSGRLLAGYDDFNCLNDAMKGDRAGVLAGHDNR	QY	315 VSCLGVTDGMAVATGSMDSFLKIWN 340	340	326
Db	301 VSCLGVTDGMAVATGSMDSFLKIWN 326	QY	301 VSCLGVTDGMAVATGSMDSFLKIWN 326	326	326

Db	181 MGHIGDCMSLAVSPDFRLFVSCACDATAKLUWDIRGTCROTFTGHESDINAICFFPNEA	240	OS Rattus norvegicus (Rat).
Qy	241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM	300	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM	300	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Qy	: : : : : : : : : : :	[1]	NCBI_TAXID=10116;
Db	301 KSERVGLSLGHDRNRSCLGVTADGMAVATGSWDSFLKIWN	340	RN [1]
301 KSERVGLSLGHDRNRSCLGVTADGMAVATGSWDSFLKIWN	340	RP SEQUENCE FROM N.A.	
RESULT 2			RC STRAIN="SPRAGUE-DAWLEY";
QDFHO			RA Wang X.B.; Funada M.; Imai Y.; Revey R.S.; Ujike H.; Vandenbergh D.J.;
ID QDFHO			Uhl G.R.; "rgb1: A psychostimulant-regulated gene essential for establishing cocaine sensitization";
AC QDFHO:			Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DT 01-MAR-2001 (TREMBIrel. 16, Created)			DR EMBL; U88324; AD00650.1; -.
DT 01-MAR-2001 (TREMBIrel. 16, Last sequence update)			DR HSSP; P04901; ITBG.
DT 01-MAR-2001 (TREMBIrel. 16, Last annotation update)			DR InterPro; IPR00532; -.
DR G-PROTEIN B1 SUBUNIT			DR InterPro; IPR001680; -.
OS Ambystoma tigrinum (Tiger salamander).			DR Pfam; PF00400; WD40; 7.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DR PRINTS; PRO0319; GPROTEINB.
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;			DR PROSITE; PS00320; GPROTEINBRPT.
OX NCBI_TAXID=8305;			DR SMART; SM00320; WD40; 1.
RN [1]			KW repeat; WD repeat.
RP SEQUENCE FROM N.A.			SEQUENCE 340 AA; 37387 MW; D9EBE6B0FF7EC57 CRC64;
RC TISSUE=RETINA;			Query Match
RT "Cloning and Characterization of G-protein Beta subunits from the			Best Local Similarity 87.1%; Score 1575; DB 13; Length 340; Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;
RL Salamander Retina;"			Qy 1 MGEMEQLRQEAEQKLQDADAKACADVTLAELSGLEVLGVGRVOMRTRTLRHLAKIYA 60
DR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			Db 1 MSELEQOLRQEAEQKLQDADAKACADVTLAELSGLEVLGVGRVOMRTRTLRHLAKIYA 60
SQ SEQUENCE 340 AA; 37332 MW; 84E1451RBD83D8F3 CRC64;			Qy 61 MHAWTDKSLVSAASODKLWIVDSYNTNKHAIPURSSWMTCAYAPSGNFWVACGGIDNM 120
Query Match	87.1%; Score 1575; DB 13; Length 340; Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;		Db 61 MHAWTDKSLVSAASODKLWIVDSYNTNKHAIPURSSWMTCAYAPSGNFWVACGGIDNM 120
Qy 1 MGEMEQLRQEAEQKLQDADAKACADVTLAELSGLEVLGVGRVOMRTRTLRHLAKIYA 60			Qy 121 CSYLNKASREGKVVKVRSRELHTGVLSCCREFLDDNNITVSSGTTCALWDIETGQOKTVF 180
Db 1 MSELEQOLRQEAEQKLQDADAKACADVTLAELSGLEVLGVGRVOMRTRTLRHLAKIYA 60			Db 121 CSYLNKASREGKVVKVRSRELHTGVLSCCREFLDDNNITVSSGTTCALWDIETGQOKTVF 180
Qy 61 MHAWTDKSLVSAASODKLWIVDSYNTNKHAIPURSSWMTCAYAPSGNFWVACGGIDNM 120			Qy 181 VGHGDGMSLAVSPDNLETSGACASAKLWDIRGTCROTFTGHESDINAICFFPNEA 240
Db 61 MHAWTDKSLVSAASODKLWIVDSYNTNKHAIPURSSWMTCAYAPSGNFWVACGGIDNM 120			Db 181 TGTGDMVMSLAPDTRFLVSGACASAKLWDIRGTCROTFTGHESDINAICFFPNEA 240
Qy 121 CSYLNKASREGKVVKVRSRELHTGVLSCCREFLDDNNITVSSGTTCALWDIETGQOKTVF 180			Qy 241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM 300
Db 121 CSYLNKASREGKVVKVRSRELHTGVLSCCREFLDDNNITVSSGTTCALWDIETGQOKTVF 180			Db 241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM 300
Qy 181 VGHGDGMSLAVSPDNLETSGACASAKLWDIRGTCROTFTGHESDINAICFFPNEA 240			Qy 301 KSERVGLSLGHDRNRSCLGVTADGMAVATGSWDSFLKIWN 340
Db 181 VGHGDGMSLAVSPDNLETSGACASAKLWDIRGTCROTFTGHESDINAICFFPNEA 240			Db 301 NADRAGVLAGHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
Qy 241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM 300			Result 4
Db 241 ICGSDDASCRFLDRADQELCFSHESICGITSVAFLSGRLFAGYDFNCNVWDSM 300			QSHAVO
Qy 301 KSERVGLSLGHDRNRSCLGVTADGMAVATGSWDSFLKIWN 340			ID QSHAVO PRELIMINARY; PRT; 340 AA.
Db 301 KSERVGLSLGHDRNRSCLGVTADGMAVATGSWDSFLKIWN 340			AC QSHAVO;
RESULT 3			DT 01-MAR-2001 (TREMBIrel. 16, Created)
Q9QKB			DT 01-MAR-2001 (TREMBIrel. 16, Last sequence update)
ID Q9QKB			DT 01-MAR-2001 (TREMBIrel. 16, Last annotation update)
AC Q9QKB;			DR GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 4.
DT 01-MAY-2000 (TREMBIrel. 13, Created)			GN GNB4.
DT 01-MAR-2001 (TREMBIrel. 13, Last sequence update)			OS Homo sapiens (Human).
DE G PROTEIN BETA SUBUNIT.			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RGB1;			OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
			NCBI_TAXID=9605;
			RN [1]
			RP SEQUENCE FROM N.A.
			RA Puhl H.L., III, Ikeda S.R., Aronstam R.S.;
			RT "Cloning and Characterization of Human G-Protein Beta 4.";
			RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
			DR AF300648; AACG18442.1; -.

RESULT 7
 ID Q9HFS3 PRELIMINARY; PRT; 347 AA.
 AC Q9HFS3;
 DT 01-MAR-2001 (T=EMBLrel. 16, Created)
 DT 01-MAR-2001 (T=EMBLrel. 16, Last sequence update)
 DR GQUANTINE NUCLEOTIDE-BINDING PROTEIN, BETA SUBUNIT.
 SQ Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 OX NCBI_TaxID=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puri V., Park J.G., Limper A.H., Thomas C.F. Jr.;
 RT "The Pneumocystis carinii guanine nucleotide-binding protein beta
 submitted." (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF06555; ARG22770.1; -.
 SEQUENCE 347 AA; 38438 MN; FEEI495006E24882 CRC64;

Query Match 67.8%; Score 1226.5; DB 3; Length 347;
 Best Local Similarity 66.9%; Pred. No. 1.5e-106;
 Matches 222; Conservative 47; Mismatches 62; Indels 1; Gaps 1;

QY 9 QEAQDQLKQIADARKACADVTAAELVSGLEYVGRVQMRTRTLRGLAKIYAMHNATDK 68
 Db 15 KEEYLKIKIKKKDEADNLRSMAOTLVDYERLJSIRVRYTLRGLAKIYAMHNATDK 74
 QY 69 LLYVASQDQKLIVWDTSYTNKWHAIPLRSSWMTCAVAPSGNFVACAGGLDNMCSTYNLS 128
 Db 75 HLVYASQDQKLIVWDTSYTNKWHAIPLRSSWMTCAVAPSGNFVACAGGLDNMCSTYNLS 134
 QY 129 REGNVKVSRELSAHTGVLSCRCFLDNNIVSSGGTCAWIDFREGQQKIVFVGRTGDM 188
 Db 135 KDGHAKTARELMAHTGVLSCRCFLDQIULSSGMSCILWDINGSKQFEFLDHLDGDM 194
 QY 189 SLAVSP-DFLNFTSACDASAKLWDVREGTCRQTFGHESDINATCFFPGEAICTGSDD 247
 Db 195 SLSIHPNPNLNEVGACDARKKINDRIGSVQTEAGHESDINAQWQIFPNNAFATGSDD 254
 QY 248 ASCRFDLRADQELLCFSHEISICGITSVAFSLSRLLPAGYDFNCNWMSKSERGI 307
 Db 255 ASCRFDLRADQELLCFSHEISICGITSVAFSLSRLLPAGYDFNCNWMSKSERGI 314
 QY 308 LSGHDNNSVCLGVTADGMATGSDSELEK1W 339
 Db 315 LGQHNDRNVSCVGVSKDGRSLATGSWDSLKIW 346

RESULT 8
 ID Q9W3J1 PRELIMINARY; PRT; 352 AA.
 AC Q9W3J1;
 DT 01-MAY-2000 (T=EMBLrel. 13, Created)
 DT 01-MAY-2000 (T=EMBLrel. 13, Last sequence update)
 DE G-PROTEIN BETA SUBUNIT.
 GN SPAD.
 OS Emericella nidulans (*Aspergillus nidulans*).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 RN NCBI_TaxID=5072;
 RN [1];

SEQUENCE FROM N.A.
 RA Rosen S., Yu J.-H., Adams T.H.;
 RT "Aspergillus nidulans fibA suppressor sfAD identifies the G-beta
 subunit of a heterotrimeric G protein";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF056182; AAC033436.1; -.
 DR HSSP: P04901_1TBG.
 DR InterPro: IPR001632; -.
 DR MEDLINE=10731132;
 DR PRINS; PR00320; GROTEINNB.
 DR PROSITE; PS00578; WD_REPEATS; UNKNOWN_3.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 352 AA; 38888 MN; 186A16886B4DF466 CRC64;

Query Match 67.4%; Score 1219.5; DB 3; Length 352;
 Best Local Similarity 64.6%; Pred. No. 6.9e-106;
 Matches 223; Conservative 50; Mismatches 65; Indels 7; Gaps 3;

QY 2 GEMPO----LRLRQEAEQIKKQIADARKACADVTAAELVSGLEVYGRVQMRTRTLRGL 55
 Db 6 GEHQQAQTAAARRRRAEGLKDKTRRKDQDLMTRLTVQANQMDALPRIGMKPRRIKGH 65
 QY 56 AKIYAHMWAATDSKLVSASQDKLIVWDSYNTKWHAIPLRSSWMTCAVAPSGNFVACG 115
 Db 66 AKIYAHMWAATDSKLVSASQDKLIVWDSYNTKWHAIPLRSSWMTCAVAPSGNFVACG 125
 QY 116 GLDNMCSTYNLSREGNKVKSPELSAHTGVLSCRCFLDNNIVSSGGTCAWIDFREGQQKIVFVGRTGDM 175
 Db 126 GLDNMCSTYNLSREGPTRYRVARELSGHSGLSICRCFRINDRITTSGGDMCMLWDIESGS 185
 QY 176 QKTFADFGDMSISINPTMNQIFVSGACDAFKLWDRTGKAVQTFGHESDINATOF 234
 Db 186 KTFEFADFGDMSISINPTMNQIFVSGACDAFKLWDRTGKAVQTFGHESDINATOF 245
 QY 235 FPGEEATCTGSDASCRFLDRADQELICSHESICGITSVAFSLSGRLFAGYDFNC 294
 Db 246 FPDGNAFTGTSQSLDTTCRLFDIADRALSNTYOSDQIICGITSVAFSVERLFAGYDFEC 305
 QY 295 NWDSMSKSERGIVLSDHNRVSCLVGTADGMATGWSWDSLKIW 339
 Db 306 KWDVLRGDVKVGSLSGHENRVSCLVGSNGISLOTGSMWDSLKIW 350

RESULT 9
 ID Q9W3J1 PRELIMINARY; PRT; 358 AA.
 AC Q9W3J1;
 DT 01-MAY-2000 (T=EMBLrel. 13, Created)
 DT 01-MAY-2000 (T=EMBLrel. 13, Last sequence update)
 DE G-PROTEIN BETA SUBUNIT.
 DE CG10763 PROTEIN.
 DE CG10763.
 OS Drosophila melanogaster (Fruit fly).
 OC Drosophila; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Pterygota; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=10731132;
 RA Adams M.P., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amatiades P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Peeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brostoff P., Brottier P.,
 RA Burts K.M., Busam D.A., Butler H., Cadle E., Center A., Chandra I.,
 RA Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeawam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod J., Scheeler F., Shen H.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
 RA Nelson R., Nelson K.A., Nixon K., Nuuskern K., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinhart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stadelton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL *Science* 2001;287:2185-2195(2000).
 EMBL: AE003443; AAF6336.1; -. .
 DR HSSP: P04501; ITBG;. .
 DR FlyBase: FBgn0030011; CG10763;. .
 DR InterPro: IPR0016320; -. .
 DR Pfam: PF00400; WD40;. .
 DR PRINTS: PR00320; PROTEINBPR.
 DR PROSITE: PS00678; WD_REPEATS;. .
 DR SMART: SM0320; WD40;. .
 DR SWISSPROT: WD40;. .
 KW SEQUENCE 358 AA; 39354 MW; E9G6DEF91C503231 CRC64;

 Query Match 53.5%; Score 967.5; DB 5; Length 358;
 Best Local Similarity 50.0%; Prcd. No. 2.5e-82;
 Matches 170; Conservative 78; Mismatches 89; Indels 3; Gaps 2;
 Qy 3 EMEQIQRQEQLKQIQAIDARRACAVTIAELVSGLEVGRQMRTRRTHIKAQTYAH 62
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 18 KMASIVREALENKTYKLEERBKLNQNLNSIAELEQIAVNYNTPRKVLKGHOAKVLCTD 77

 Qy 63 WATDSKLVLVASODQGKLWDSYNTVKHIAPIPLRSWVTCATAPSGNFWAGGLDNMCS 122
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 78 WSPKRHTISSLSSQDRLITDAFTINKERHAVIMETIWIMACATAPSGNFWAGGLDNKVT 137

 Qy 123 TYNIKSREGNVKVSRELSAHTGYISCCREL-D-NNNTVSSGDTCAIMDIEGQQKAVFY 181
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 138 VYPITSDDEEMAAKKRTVGHTYSMSCC1YPSNDQOQILNGSGDSMCALMDVESQLOSPH 197

 Qy 182 GHTGCMMSLAVSPD--FNEIGSADASQKLVWREGICROTIGHESDINAFCFFG 239
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 198 GHSGVMAIDALPNETGNFTVFSGCDRAFIWDMRSGHWQSFEGHQSDVNSKFHCQGD 257

 Qy 240 AICGSDDASCRQEDLRADQELICFFSHHSIICGTSVAFSLSGRLLAGYDDENCWDS 299
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 258 ALANGSDSOSCRLLMDRADREVAFKAKSISICGVNSDSESGRLLAGYDDINDVW 317

 Qy 300 MKSERVGLSLGDHNDRVNSCLGVTADGMAYATGSMDFKIRV 339
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 318 LKSERVCLLYGHENKVSCVQNSPDGTALSTGSNDYTIRVW 357

RESULT 10
 Q9HAU9 PRELIMINARY; PRT; 395 AA.
 ID Q9HAU9
 AC Q9HAU9;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 5L
 GN GNBS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puh H.L. III; Ikeda S.R., Aronstam R.S.;
 RT "Cloning and characterization of human G-protein beta 5L subunit.";
 RL Submitted (Aug 2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF00650; AAC18444.1; -. .
 SQ SEQUENCE 395 AA; 43566 MW; E001B07FCFA587AD CRC64;

Query Match 52.5%; Score 949.5; DB 4; length 395;
 Best Local Similarity 52.2%; Pred. No. 1.e-80;
 Matches 1/8; Conservative 56; Mismatches 102; Indels 5; Gaps 3;
 Qy 4 MEDUROEAQQLKQIQAIDARRACADVTLAELVSGLEVGRQMRTRRTHIKAQTYAH 63
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 54 LASLKLSEAESLKQKLEEBRAKLIIDVELHQVAERVEALQGVFVTRPLKGHKVYLCDW 113

 Qy 64 ATDSKLVLVASODQGKLWDSYNTVKHIAPIPLRSWVTCATAPSGNFWAGGLDNMCS 123
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 114 CKDKRRTVSSDGGKVITWDSTPNTKHAVNPCTWNMACAYAPSCLACGGGLNCKSV 173

 Qy 124 YNL--KSREGNVKVSREL-SAHTGYISCCREL-DNNNTVSSGDTCAIMDIEGQQKTFV 180
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 174 YPITFDKVNEMMAKKSVAMHNYLSCSFNNSDMQILTASGDGTCALWDVESGOLQSF 233
 DR PRINTS; PR00320; PROTEINBPR.
 DR PROSITE; PS00678; WD_REPEATS;. .
 DR SMART; SM0320; WD40;. .
 DR SWISSPROT: WD40;. .
 DR TRepeat; WD repeat;. .
 SQ SEQUENCE 358 AA; 39354 MW; E9G6DEF91C503231 CRC64;

Query Match 53.5%; Score 967.5; DB 5; Length 358;
 Best Local Similarity 50.0%; Prcd. No. 2.5e-82;
 Matches 170; Conservative 78; Mismatches 89; Indels 3; Gaps 2;
 Qy 3 EMEQIQRQEQLKQIQAIDARRACAVTIAELVSGLEVGRQMRTRRTHIKAQTYAH 62
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 18 KMASIVREALENKTYKLEERBKLNQNLNSIAELEQIAVNYNTPRKVLKGHOAKVLCTD 77

 Qy 63 WATDSKLVLVASODQGKLWDSYNTVKHIAPIPLRSWVTCATAPSGNFWAGGLDNMCS 122
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 78 WSPKRHTISSLSSQDRLITDAFTINKERHAVIMETIWIMACATAPSGNFWAGGLDNKVT 137

 Qy 123 TYNIKSREGNVKVSRELSAHTGYISCCREL-D-NNNTVSSGDTCAIMDIEGQQKAVFY 181
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 138 VYPITSDDEEMAAKKRTVGHTYSMSCC1YPSNDQOQILNGSGDSMCALMDVESQLOSPH 197

 Qy 182 GHTGCMMSLAVSPD--FNEIGSADASQKLVWREGICROTIGHESDINAFCFFG 239
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 198 GHSGVMAIDALPNETGNFTVFSGCDRAFIWDMRSGHWQSFEGHQSDVNSKFHCQGD 257

 Qy 240 AICGSDDASCRQEDLRADQELICFFSHHSIICGTSVAFSLSGRLLAGYDDENCWDS 299
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 258 ALANGSDSOSCRLLMDRADREVAFKAKSISICGVNSDSESGRLLAGYDDINDVW 317

 Qy 300 MKSERVGLSLGDHNDRVNSCLGVTADGMAYATGSMDFKIRV 339
 Qy ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 318 LKSERVCLLYGHENKVSCVQNSPDGTALSTGSNDYTIRVW 357

RESULT 11
 Q9NFZ1 PRELIMINARY; PRT; 346 AA.
 ID Q9NFZ1
 AC Q9NFZ1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=7373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EYE;
 RA Schulz S., Huber A., Schwab K., Paulsen R.,
 RT "A novel Gamma isolated from *Drosophila* constitutes a visual G
 protein gamma subunit of the fly compound eye.";
 RT Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ250442; CAB76452.1; -. .

	Matches	149;	Conservative	74;	Mismatches	68;	Indels	19;	Gaps	7;
DR	InterPro; IPR001632;	-								
DR	InterPro; IPR001680;	-								
DR	PFam; PF00400; WD40;	7;								
DR	PRINTS; PR00319; GPROTEINB;									
DR	PROSITE; PS00678; WD_REPEATS;	UNKNOWN_1.								
DR	PRODOM; PD004738;	-;	1.							
DR	PROSITE; PS00678; WD_REPEATS;	UNKNOWN_1.								
KW	Repeat; WD_REPEATS;									
SEQUENCE	346 AA;	38383 MW;	0C88F33C518FAE55 CRC64;							
Query Match	45.9%;	Score 831;	DB 5;	Length 346;						
Best Local Similarity	43.7%;	Pred. No. 1.4e-69;	Mismatches	109;	Indels	2;	Gaps	1;		
Matches	148;	Conservative	80;	Mismatches	109;	Indels	2;	Gaps	1;	
QY	3 EMEQIQRQEAQOLKKQIADAARKACADVATLAVLVSGLLEVGRVQMRTRTLRGLAKIYAHM	62								
Db	7 ETQKLYDEINLENLKIQFQDDHKAKACTMQERCGMDIFKIRSSKKLKGHNKVSYH	66								
QY	63 WATDKKLVLVASODGDKLIVWDSYTNTKVAIPRSWSWMTCAVAPSGNFWACCGDLDNNCS	122								
Db	67 FAGDRHCYVGSLSQDKLILWTDWTWANKVQVPLRSKAWMVAFSPSGNFVACGGMDNOCT	126								
QY	123 IYNLKS--GNVKISRELSAHTYSLSCCRFLDNINIVSSGGDTCALDIEQOKWV	180								
Db	127 VYDVNNRNDARSGVAKMTRELLGYESFLSSCRFLDDTHLITSGDMKICHWDLEKGKTMDF	186								
QY	181 VGHTGDPMCLASLAVSPDPNLFTSGACDASKWKDVRERGTCRTGHSIDESDTNAICFPNGER	240								
Db	187 NGHADJIGLISLSPDMNTVTSVKTAKINDVREBTHKOMECHEMDYNSVCHPNSG	246								
QY	241 ICTGSDPASCLFDRADQDULCFHESIICGTAISVAFSLGRFLAGYDDFNQNVWDSM	300								
Db	247 FASASEDQTARLYDIDRAOOQIALYEPPKQKTFGTSICALSTSGRILLCSEIGNIHSDIM	306								
QY	301 KSERVGILSGDNRVSCLGVTADGIAVAVGGSWDSLKIW	339								
Db	307 KVCHNGMLQGHENRITCISLSPNGMCLASTSWDQQVRLW	345								
RESULT	12									
Q9XFK0	PRELIMINARY;	PRT;	377 AA.							
ID										
AC										
DT	01-NOV-1999 (Tremblrel. 12, Created)									
DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)									
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)									
DE	G PROTEIN BETA SUBUNIT.									
OS	pisum sativum (Garden pea).									
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;									
OC	Bakuryo; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;									
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;									
OC	Fabales; Fabaceae; Papilionoideae; Pisum.									
OX	NCBI_TAXID=3888;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=CV_ALASKA; TISSUE=APICAL BUD;									
RA	Lapik Y.R., Kaufman L.S.;									
RT	*Cloning of cDNA encoding pea G protein beta subunit.;									
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.									
DR	EMBL; AF170921; AAD49742.1;									
DR	HSSP; P04901; ITBG.									
DR	InterPro; IPR001632;	-								
DR	InterPro; IPR001680;	-								
DR	PFam; PF0040; WD40;	7;								
DR	PRINTS; PR00319; GPROTEINB;									
DR	PROSITE; PS00320; GPROTEINBPRP.									
DR	PROSITE; PS00678; WD_REPEATS;	UNKNOWN_3.								
DR	SMART; SM0320; WD40;	1.								
KW	Repeat; WD_REPEATS;									
SEQUENCE	377 AA;	40899 MW;	F4744C8C4AA32B8B CRC64;							
Query Match	45.3%;	Score 819;	DB 10;	Length 377;						
Best Local Similarity	43.4%;	Pred. No. 2.1e-58;	Mismatches	89;	Indels	36;	Gaps	9;		
Matches	157;	Conservative	80;	Mismatches	89;	Indels	36;	Gaps	9;	
QY	4 MEQIQRQEAQOLKKQIADA-----RKACADVATLAVLVSGLLEVGRVQMRTRTLRGLAKIYAHM	56								
Db	17 WNNERERLKKRQLSLDIDIAVARSQGRVPR-----GPDIICCTQHGTG	66								
QY	57 KIYAHWATDKKLVLVASODGDKLIVWDSYTNTKVAIPRSWSWMTCAVAPSGNFWACCGDLDNNCS	116								
Db	67 KVSLDWTSKKNRIVASODGDKLIVWDSYTNTKVAIPRSWSWMTCAVAPSGNFWACCGDLDNNCS	126								
QY	117 LDNMGSIYNIKS---REGNVKVSRELSAHTYSLSCCREL--DDNNIVTSGGDTCALWDI	171								

Query Match 45.4%; Score 820.5; DB 10; Length 377;
 Best Local Similarity 48.1%; Pred. No. 1.5e-68;

Db 127 LDSVCSIFNNSPFDROONLNVSRMISGHKGKVYSSQVPGEDPHLTGSGQTCVLWDI 186
 Qy 172 ETGQKTVF----VGHDGDSNLAYS-PPEFLNTSACDASAKLWYREGT-CRFTFG 224
 Db 187 TTGLRTSVFEGFRQSGHTADVLISINGSNSKLFVSGSCDAARLWTRVASRAVTFHG 245
 Qy 225 HESDNACFCFNGAICGTSDDASCRELDLRADQELTCFS---HESIICGITSVAFSL 281
 Db 247 HEQDVNSVKEFPDGNGRFQGSGSDGSCDLCRLFDIRGHQIQLQVYNQHQDNEMAHVTSAFISI 306
 Qy 282 GRLLAGYDFDNCWDSKRSERV---GILSHDNKRSVCLGVTADGMVATGSGWDSLK 337
 Db 307 GRLLAGYDGCVWDMLAKVVLNLGSLONSHEGRITCLGMSADGSALCTSWDTNLK 366
 Qy 338 IW 339
 Db 367 IW 368

RESULT 14

Q9VW29 PRELIMINARY; PRT; 346 AA.
 ID Q9VW29
 AC Q9VW29
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2000 (TREMBLrel. 13, Last sequence update)
 DE GIE746 PROTEIN
 GN G-BETH-76C OR GBETH76C OR CG88770.
 OC Drosophila melanogaster (Fruit fly).
 OC Pterygota; Neoptera; Tracheata; Hexapoda; Insecta;
 Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI-TAXID=7277;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 MEDLINE=2019005; PubMed=10731132;
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 George R.A., Lewis S.E., Richardson S.E., Ashburner M., Galle R.F.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers J.H.-C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.B.,
 Abril J.F., Abayaini A., Ao H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Bernman B.P., Bhandari D., Bolshakov S.,
 Borrova D., Botchan M.R., Bouck J., Broststein P., Brottier P.,
 Burtis K.C., Buschman D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mars A.D., Dew T., Dietz S.M.,
 Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston A.J., Hornland T.J., Wei M.-H., Hsiegawam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kraitz C., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon J., Nunes Bern D.R., Palazzolo M.,
 Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Shue B.C., Siden Kianos I., Simpson M., Skupski P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Swirskas R., Tector C., Turner R., Venter R., Venter E., Wang A.H., Wang X.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Zhang X.-H., Zhang F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Db 127 LDSVCSIFNNSPFDROONLNVSRMISGHKGKVYSSQVPGEDPHLTGSGQTCVLWDI 186
 Qy 172 ETGQKTVF----VGHDGDSNLAYS-PPEFLNTSACDASAKLWYREGT-CRFTFG 224
 Db 187 TTGLRTSVFEGFRQSGHTADVLISINGSNSKLFVSGSCDAARLWTRVASRAVTFHG 245
 DR FLYBase; FBgn004623; G-beta-76C.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40; 1.
 DR Repeat; WD repeat.
 DR Sequence; 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match

Best Local Similarity	Score	DB	Length
45.0%	814	5	346
Matches	145;	Conservative	81;
		Mismatches	11;
		Indels	2;
		Gaps	1;

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2195-2195 (2000);
 EMBL; AE003515; AAC49124; 1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001622; -.
 DR Pfam; PF00400; WD0; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00220; WD40;

4 MEQLRQEAEOLKKQIA DARKACDVTLAELVSGLEVY--GRVOMRRTTRGHIAKIYAM 61
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 17 VNDLREKLKQKRLQLD----TDVSGYARQSOKTPVTFGPTDLVCRILQHGKUHGLNM 121
 Db 62 HWATDSLKVLSASQDGKLUWVDSYTINKTHAIPIRSSWMTOAYASGNFVAACGGLDNM 131
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 72 DWTPEKRNIVASASODGRILVWNLNNTSOKHTKIPCAWMTCAFSPGSOVACGGLDNSV 131
 Db 122 STYNIKS--REGKVNVRSELAHTGYSQRCFL--DDNNIIVMSGGDTTCAALDIEGTQO 176
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 132 SFTNLMSPIDKGHNPHVPSMLSLSHKGVYSSQVYPDEDTLHILSNGDQTCVWDITPLR 191
 Db 177 KTVF----VHTGDCMSLAV--SPDFNLFISACDASAKVNDVEGT-CROFTGHRSDI 229
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 192 TSVFGEROFGSTADYQSYVSISSNPRLEVSQCDTTAGLMDTRASRQRTFYHGBCD 251
 Db 2.30 NACTCFFPNEACTGSDASCRELDRAQELICFSH--BSIGGITSVAFSLSGRILF 286
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 25.2 NTVKFSPDGNCRGTSSEDGTCLRFDRTGQLOVYQPHGDPITVSMASFSGRILF 311
 Db 287 AGYDFFENCNWDSMKSERV---GILSGHUNRVACLGVTADGMAVATGSMDSFLKIV 339
 QY || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 3112 VGISNGDCYWTDLAKTVLNLLGGVONISHGRISCLGSLSDAHCCTGSMWDTNLKIV 368

Search completed: September 28, 2001, 10:34:00
Job time: 282 sec